

1                    11    15  
 QSFG**LLDPK**    LCYLLDG--  
 5                    369  
 CD4: $\zeta$     --PTWSTPV**HADPK**    LCYLLDG--  
 369

**FIG. 1a**

1                    1  
 LGE**PQ**    LCYILDA--  
 7                    369  
 CD4: $\gamma$     --PTWSTPV**HADPQ**    LCYILDA--  
 369

**FIG. 1b**

CELL NUMBER

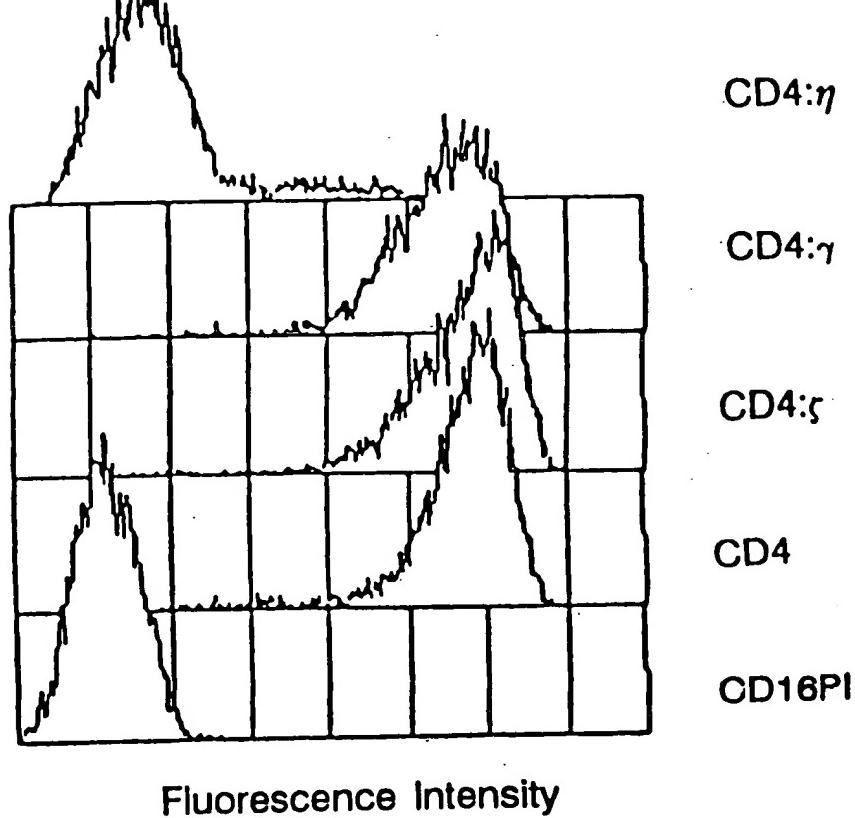
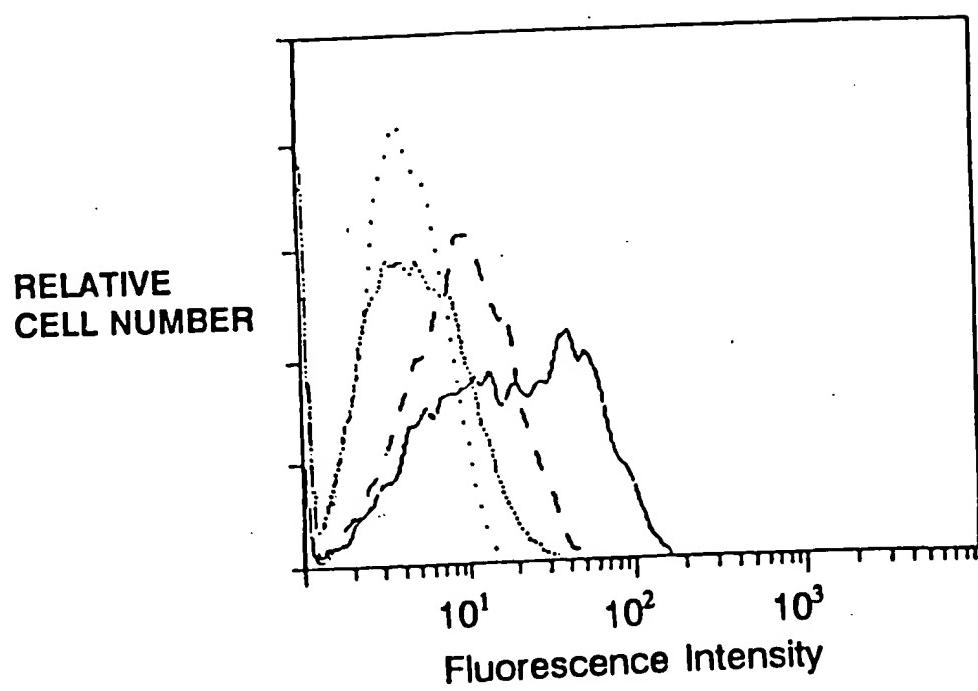
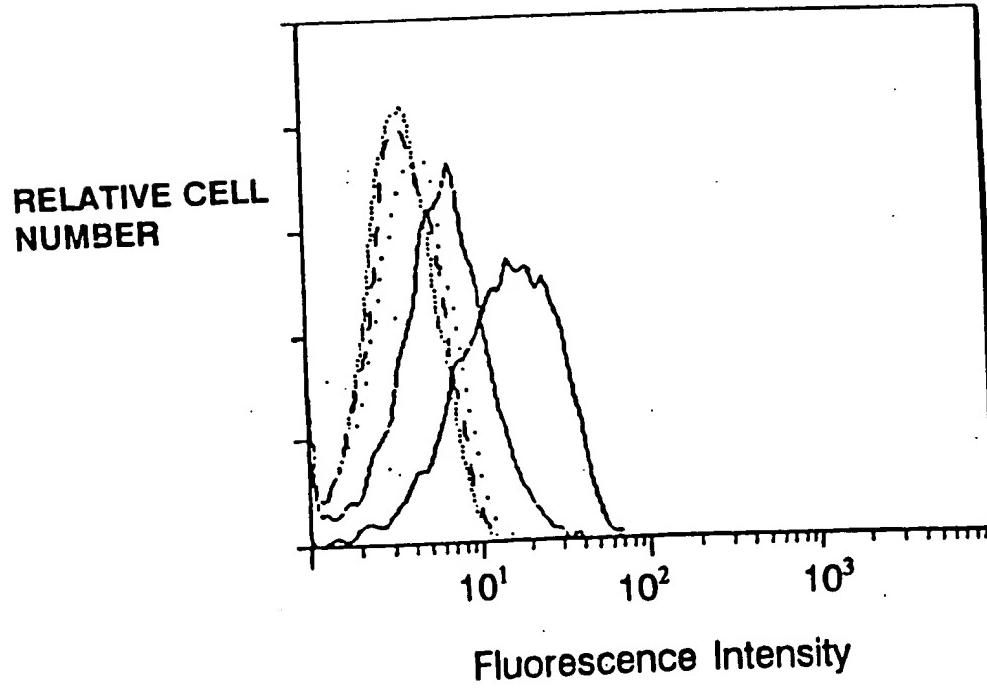


FIG. 2

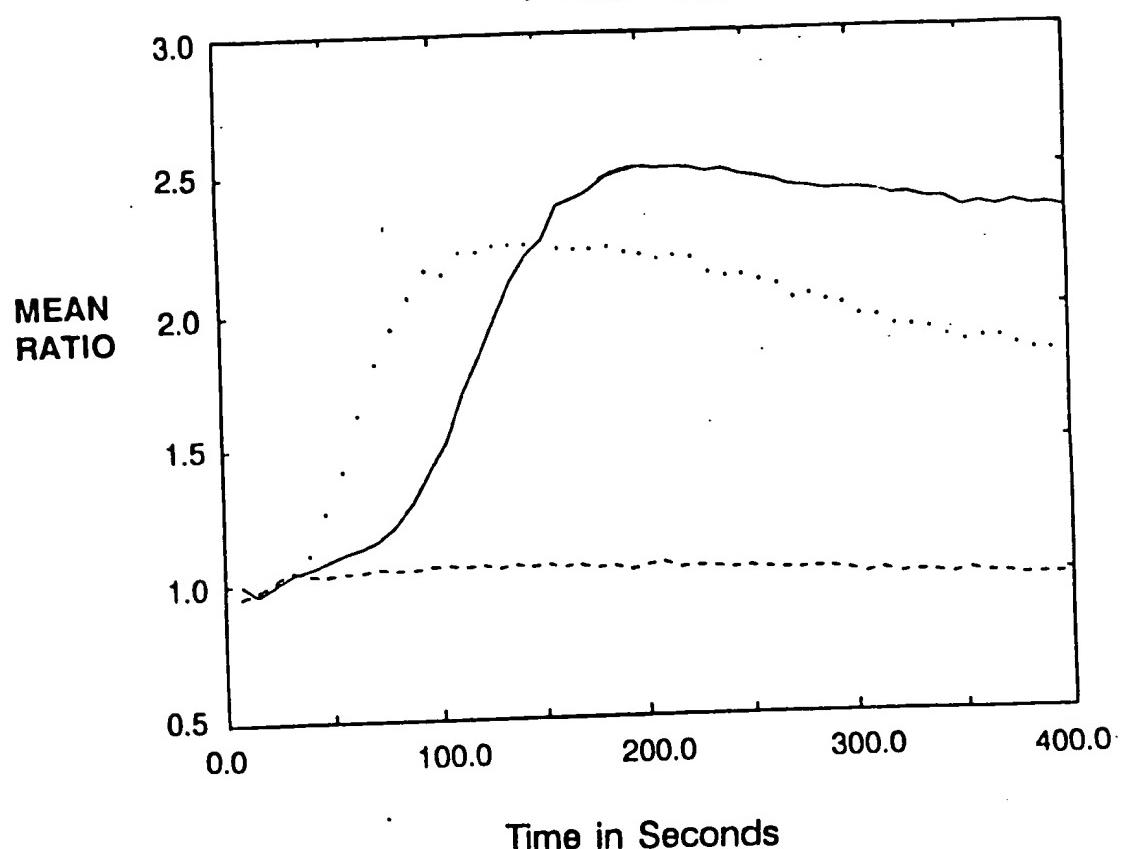


F047280 - X556660

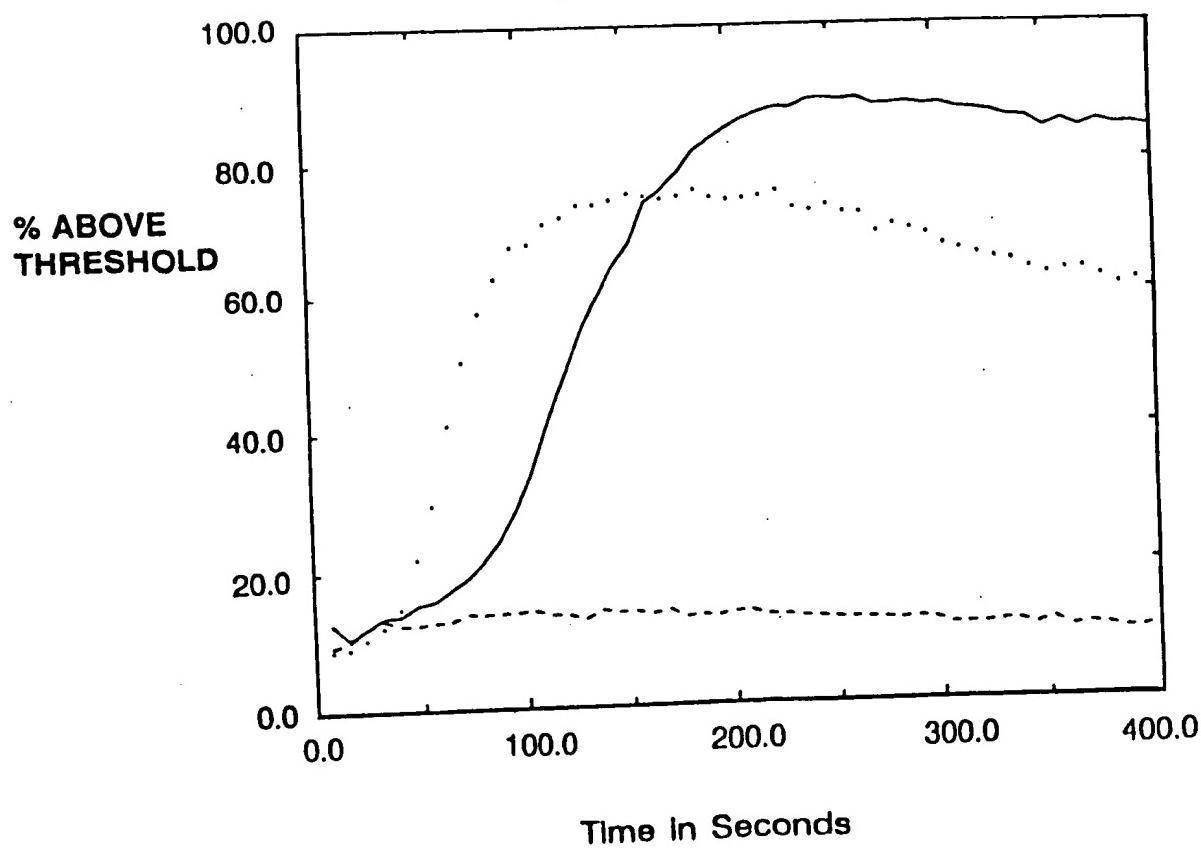
FIG. 3



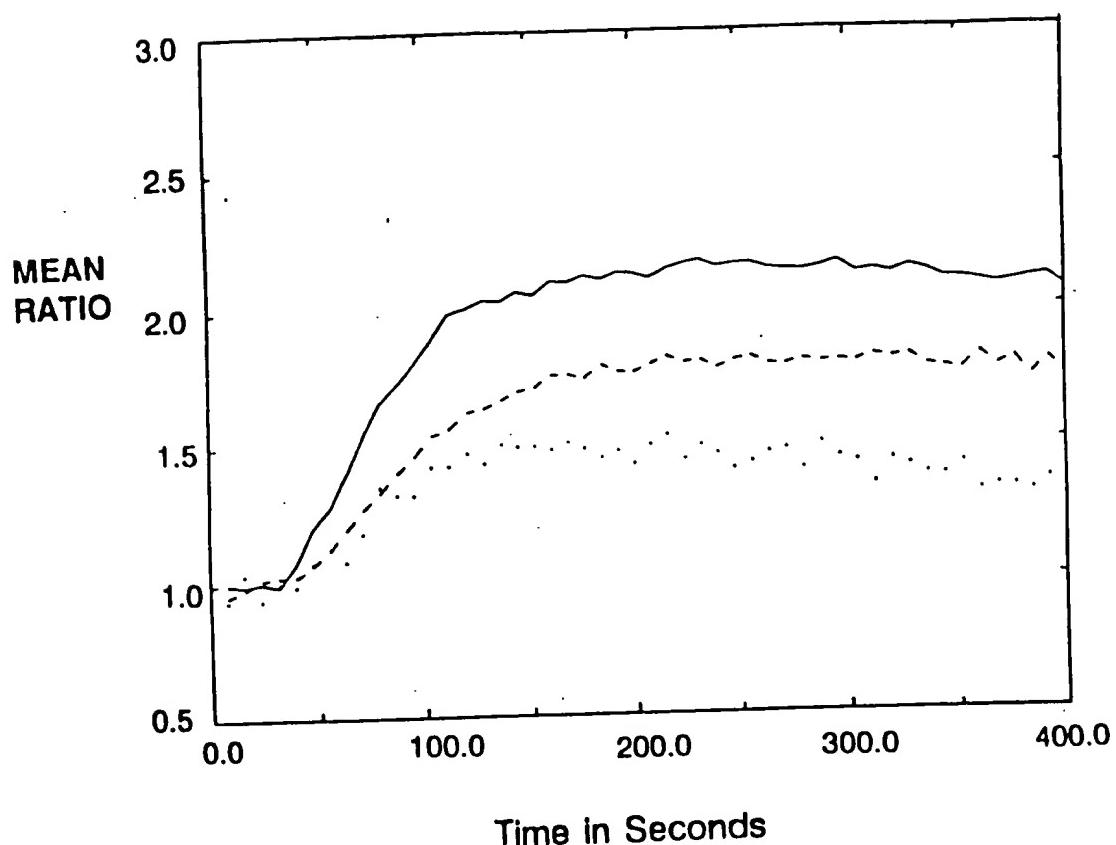
**FIG. 4a**



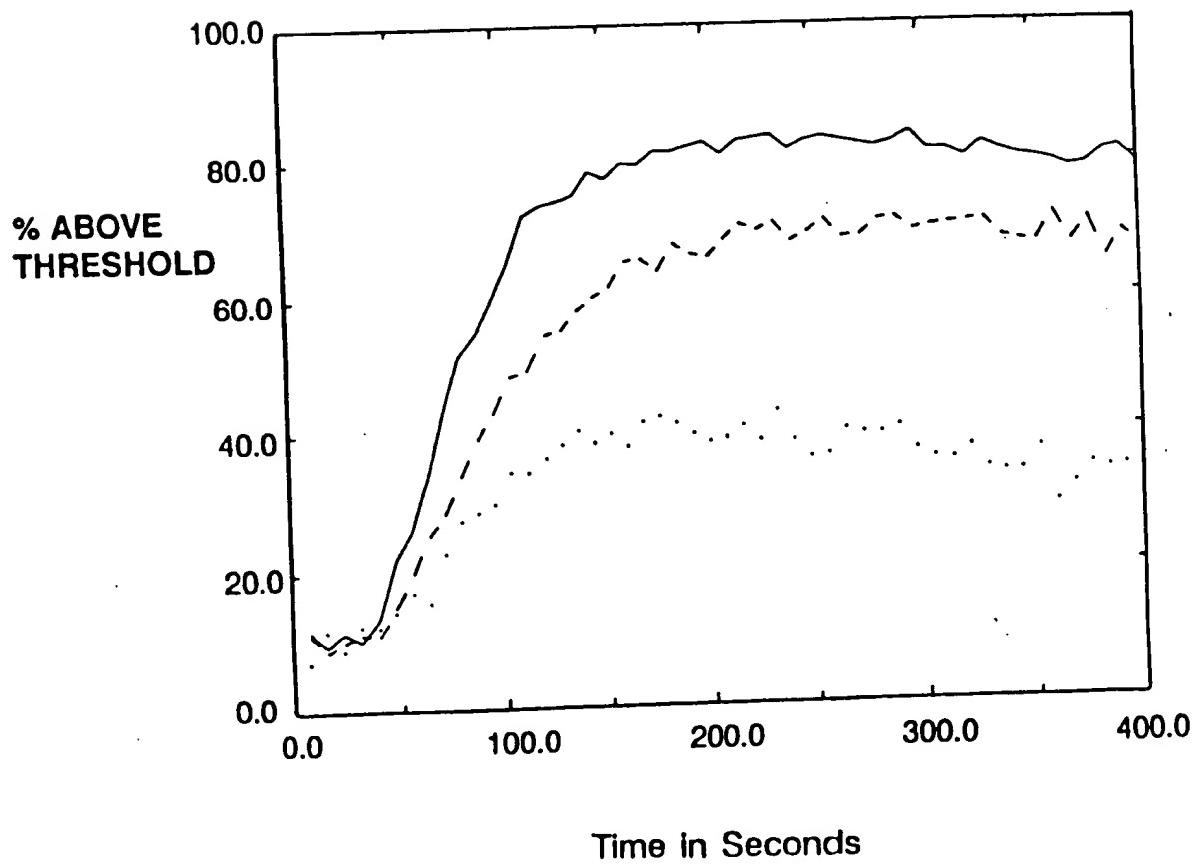
**FIG. 4b**



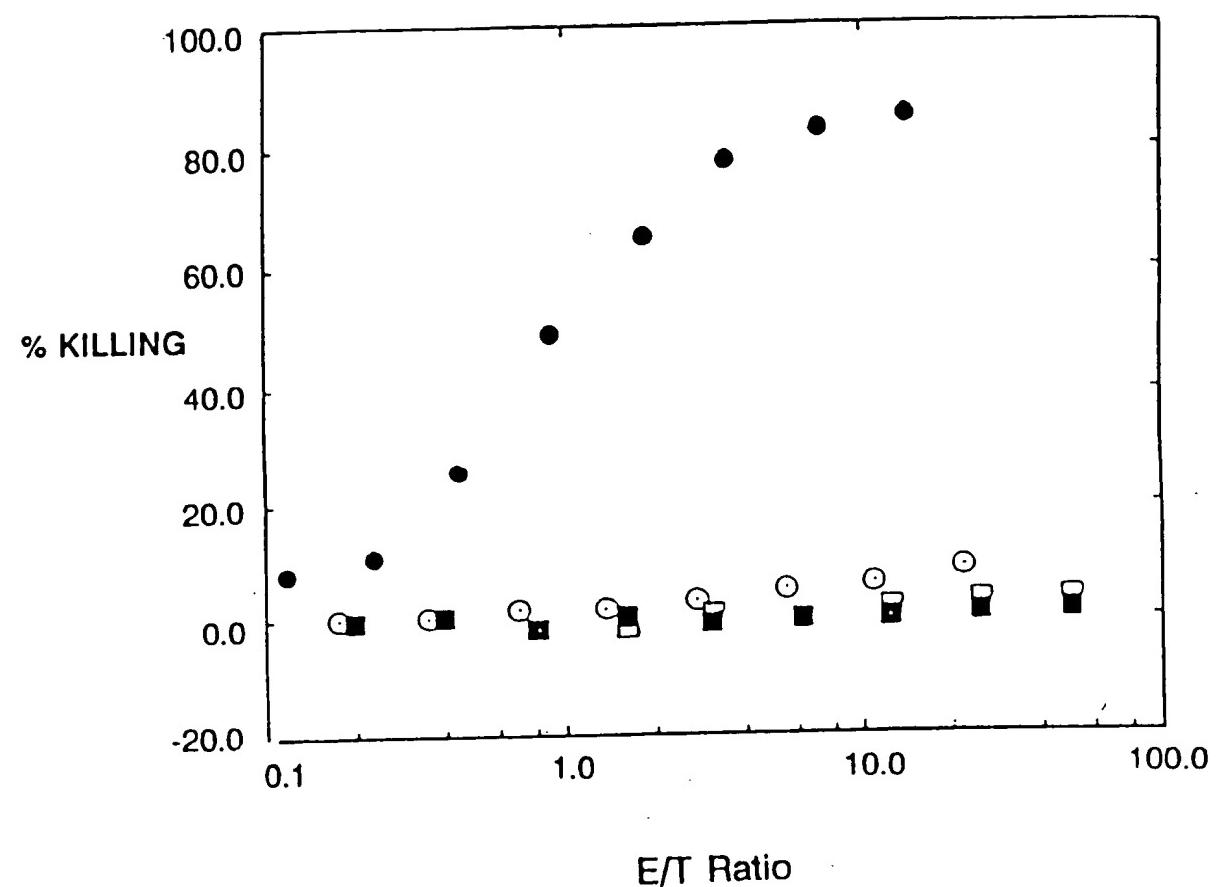
**FIG. 4c**



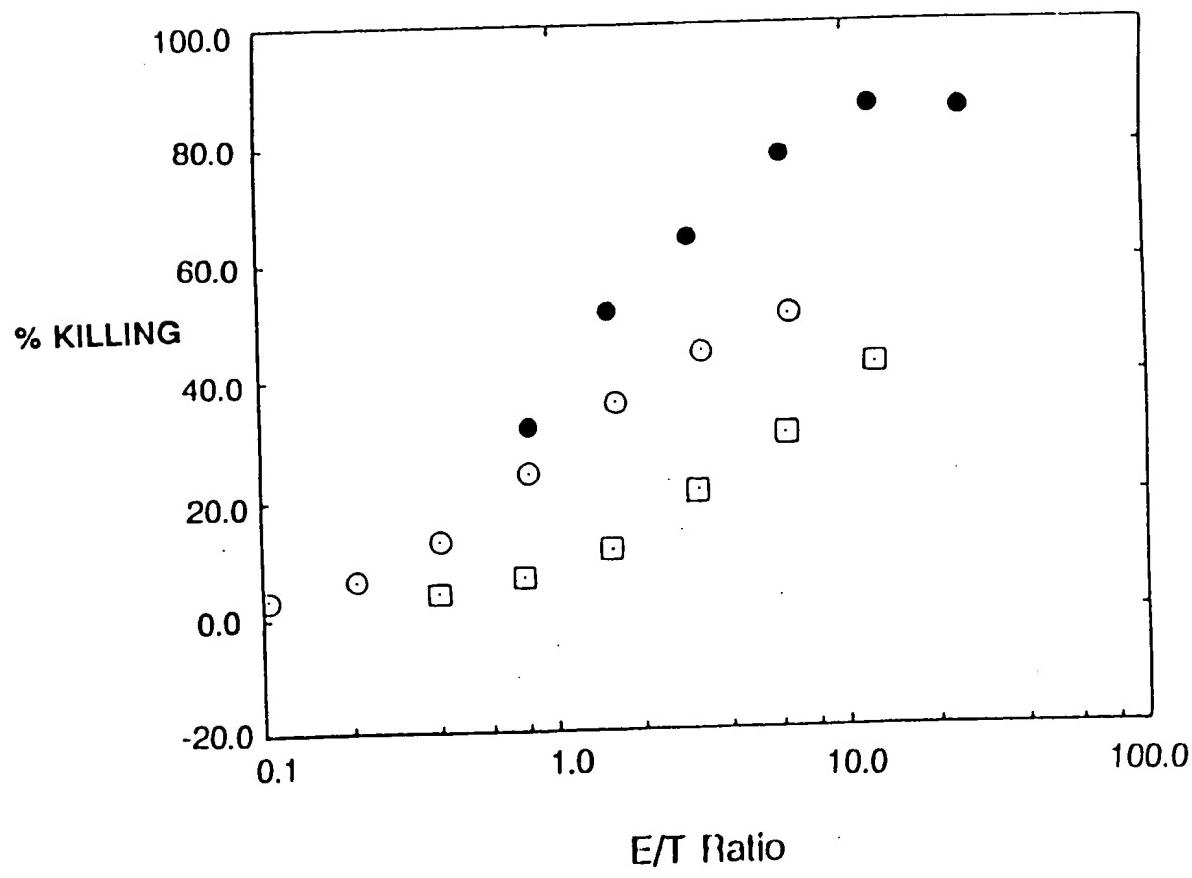
**FIG. 4d**



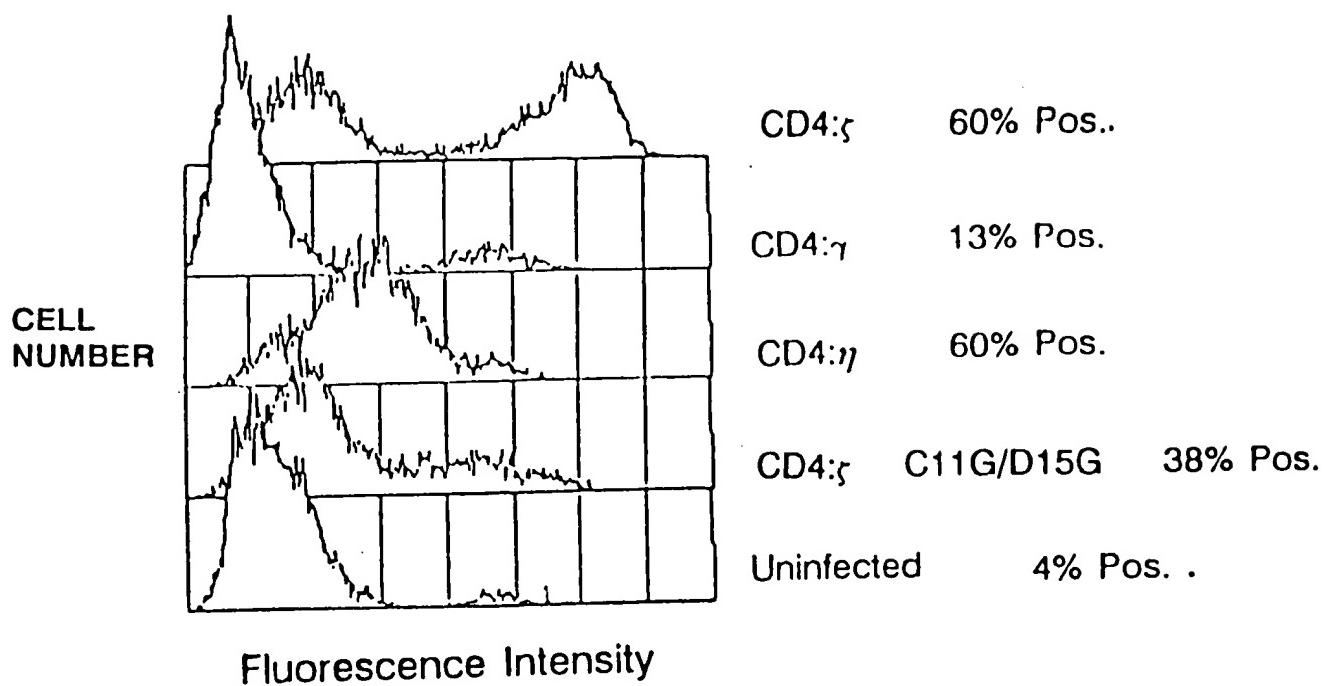
**FIG. 5a**



**FIG. 5b**

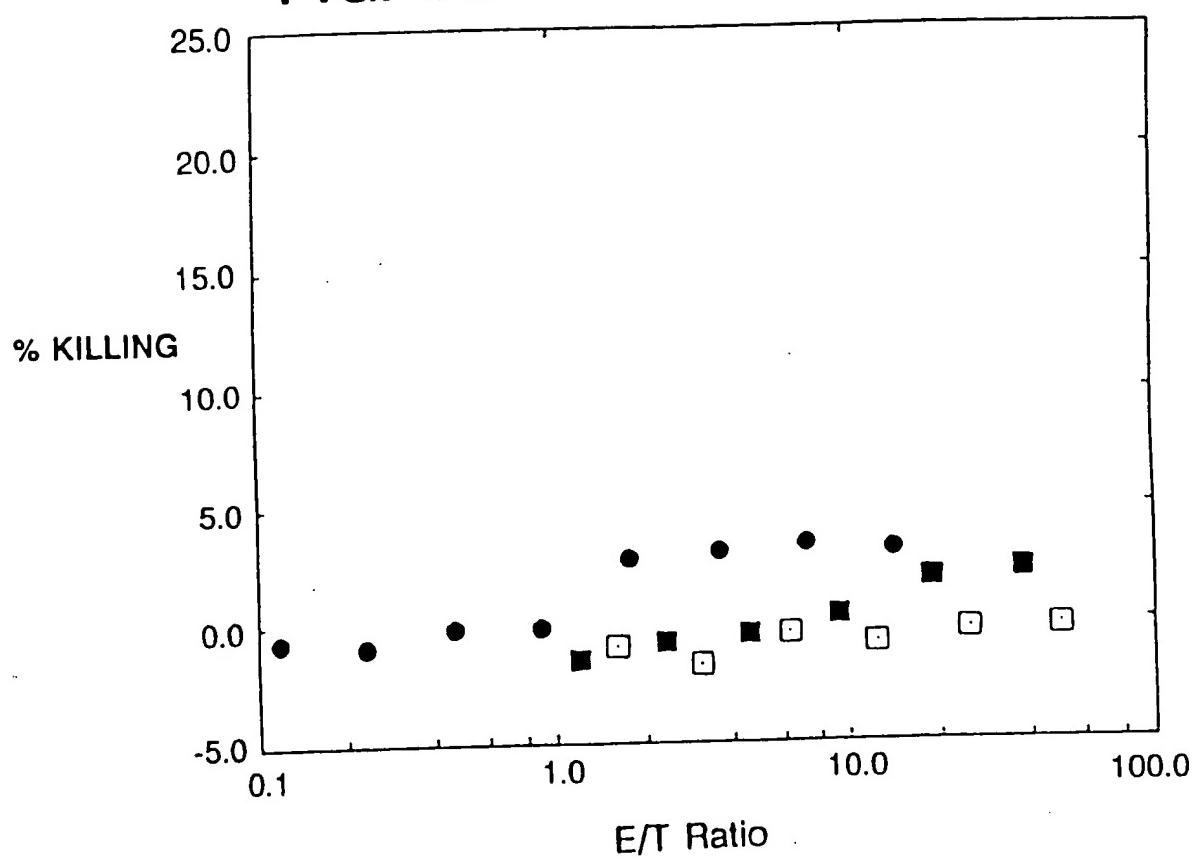


**FIG. 5c**

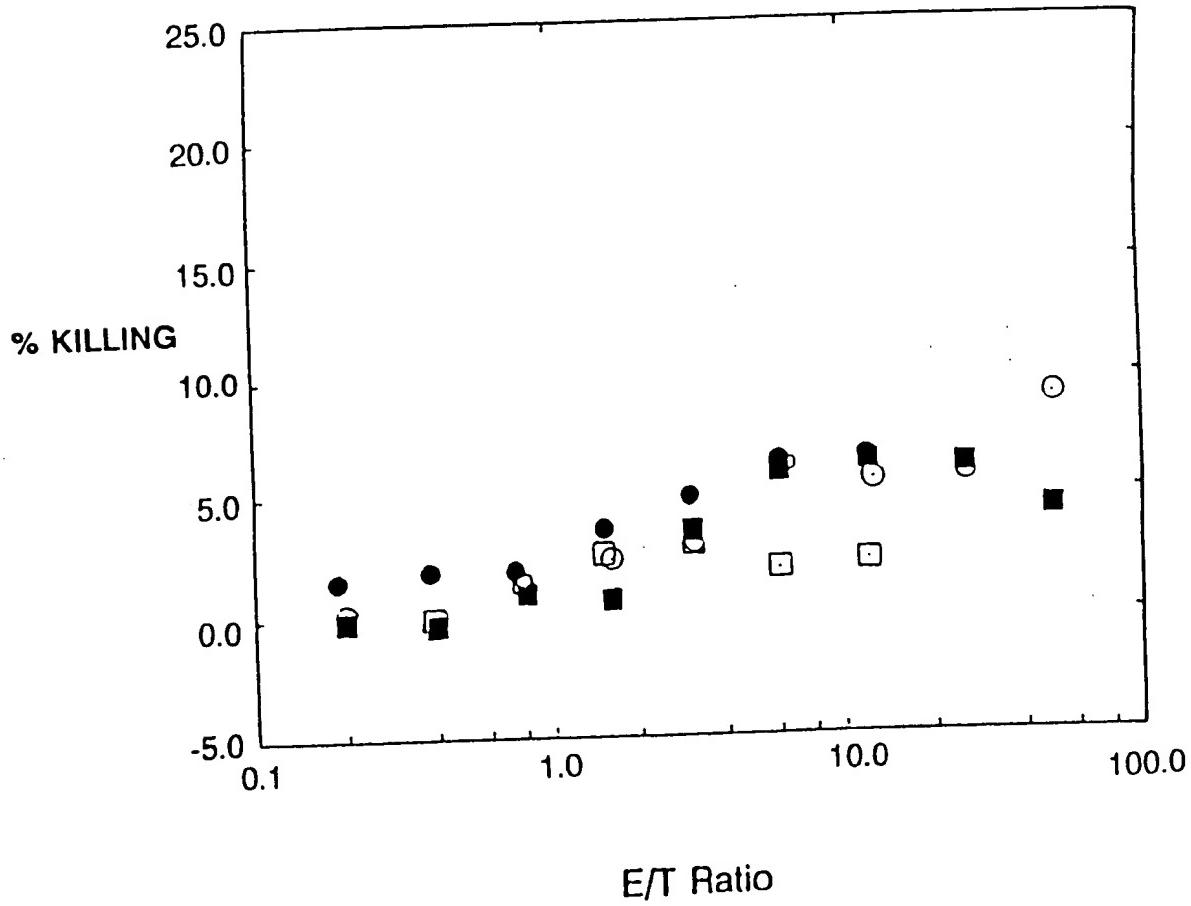


T041280 - VENUS

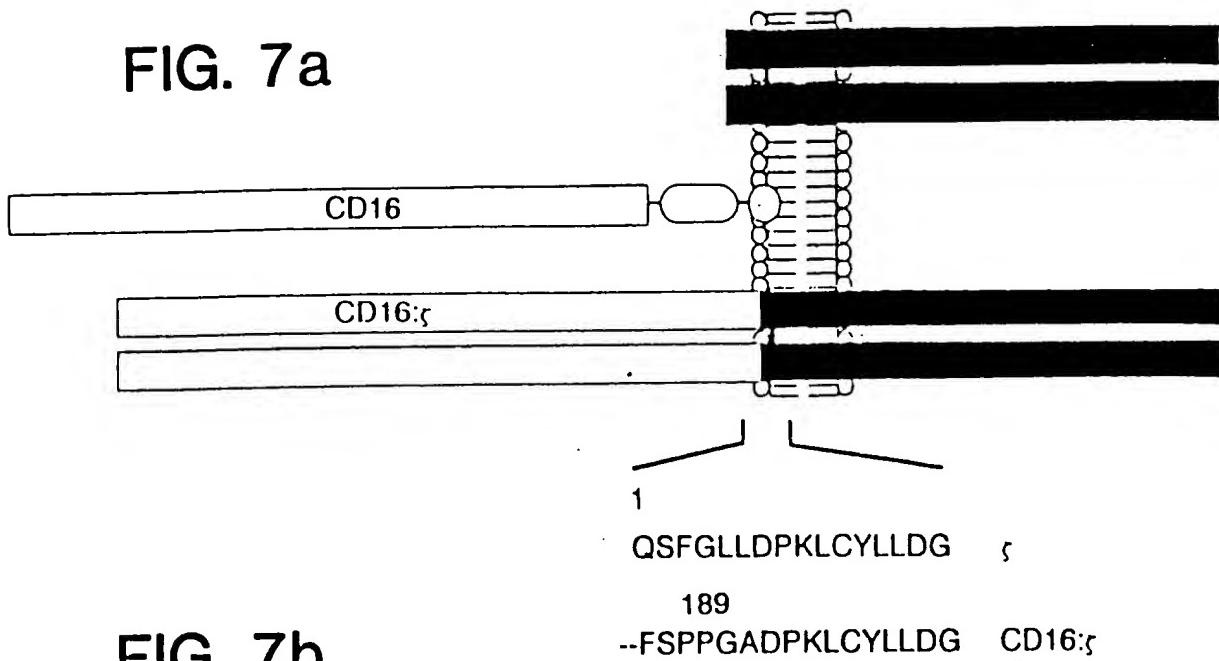
**FIG. 6a**



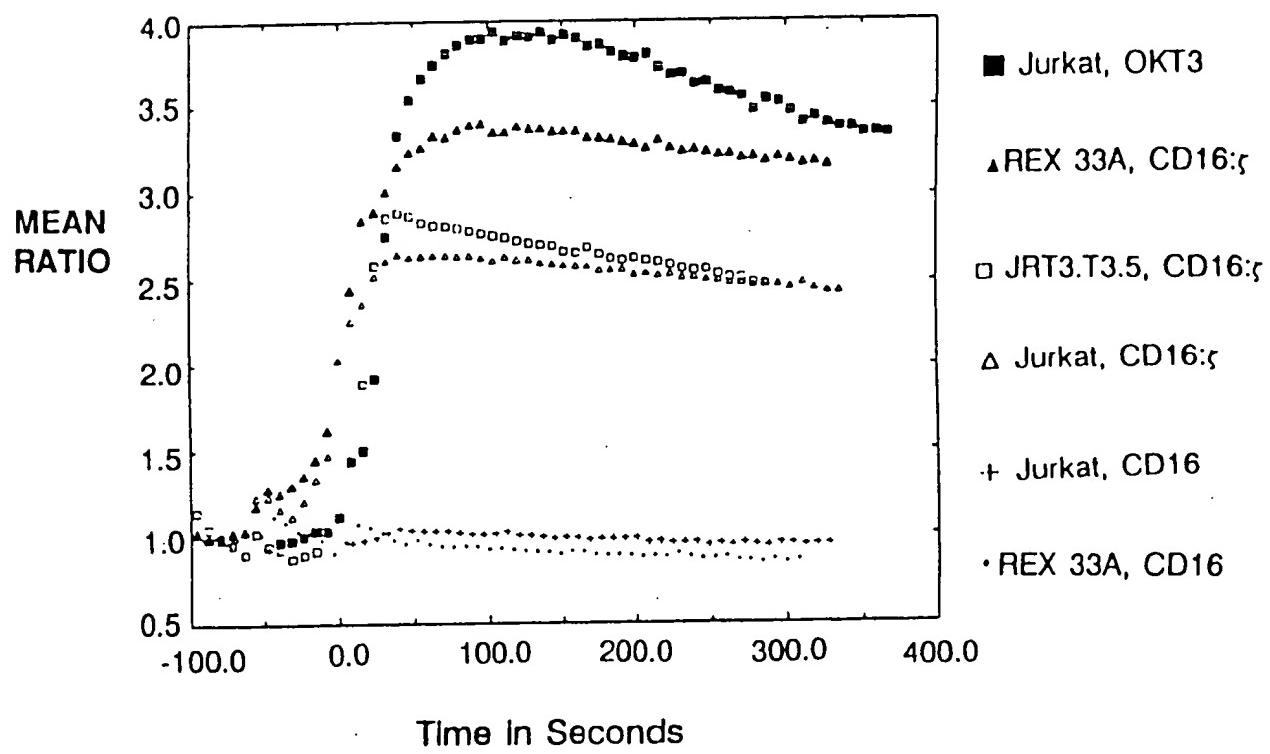
**FIG. 6b**



**FIG. 7a**



**FIG. 7b**



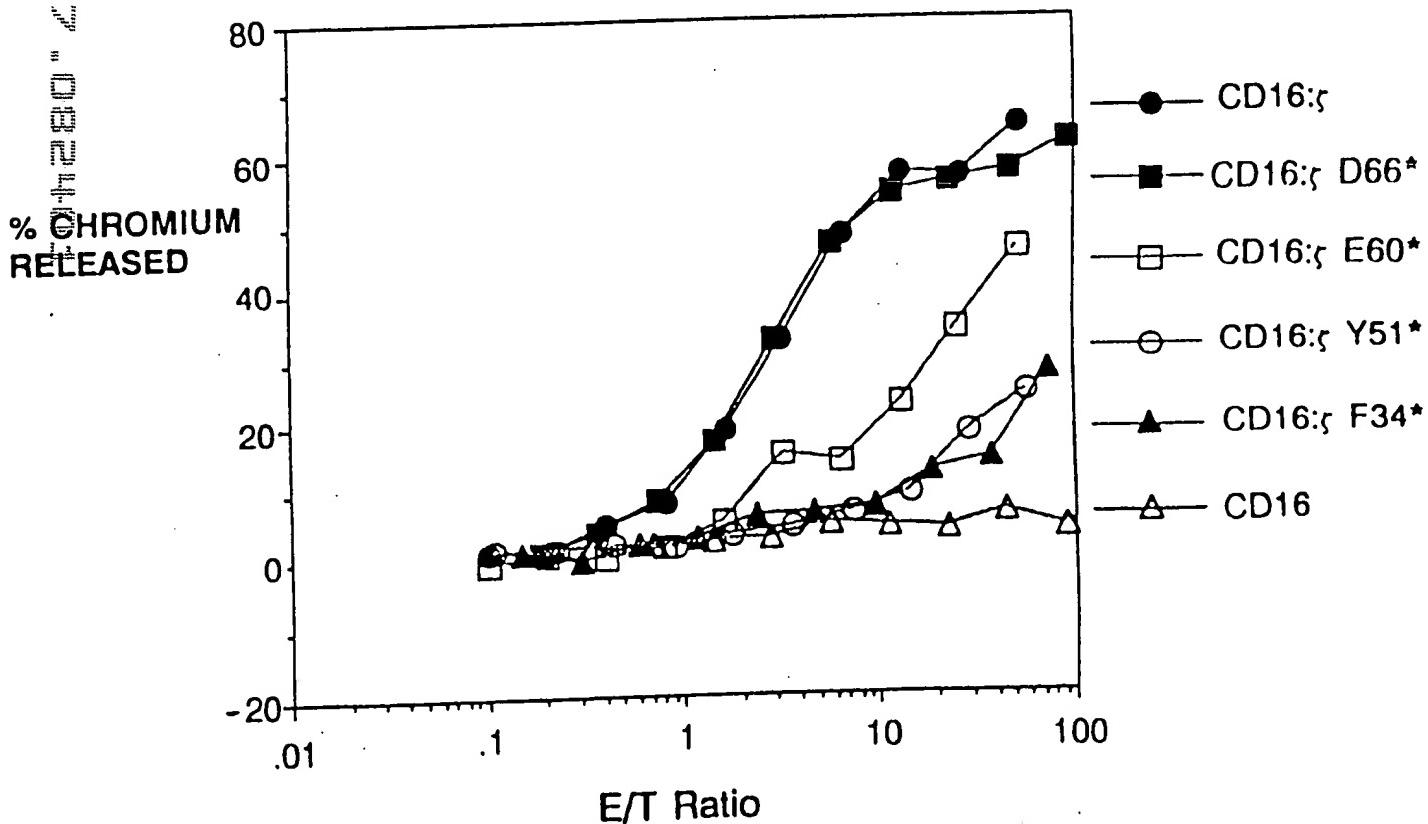
# FIG. 8a

F34\*                                    Y51\*

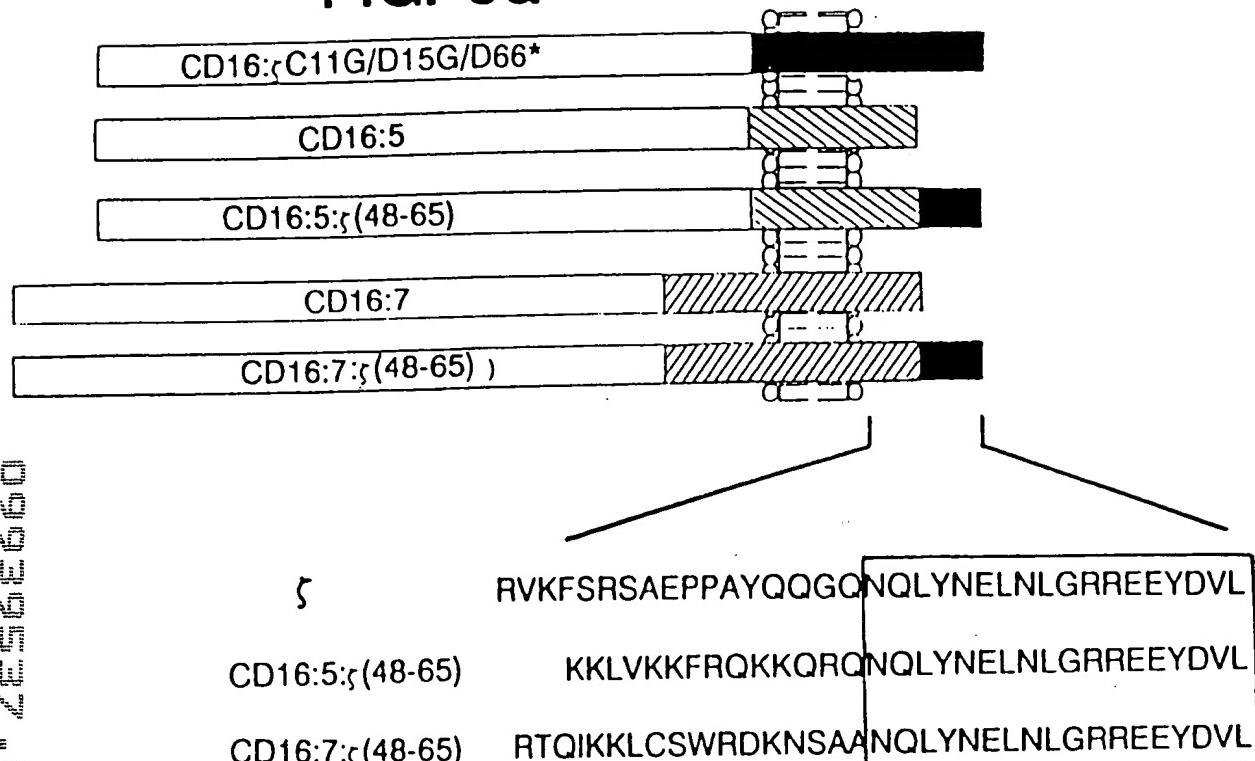
1 QSFGLLDPKL CYLLDGILFI YGVILTAFL RVKFSRSAEP PAYQQGQNQL  
 ↓                                        ↓  
 E60\* D66\*  
 51 YNELNLGRRE EYDVLVDKRRG RDPEMGGKPR RKNPQEGLYN ELQDKMAEA  
 ↓                                        ↓  
 G122\* A133\* L139\*  
 101 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR  
 ↓                                        ↓                                ↓

CD16<sup>-</sup> CD16<sup>+</sup> CD16<sup>+</sup> CD16<sup>+</sup> CD16<sup>+</sup>

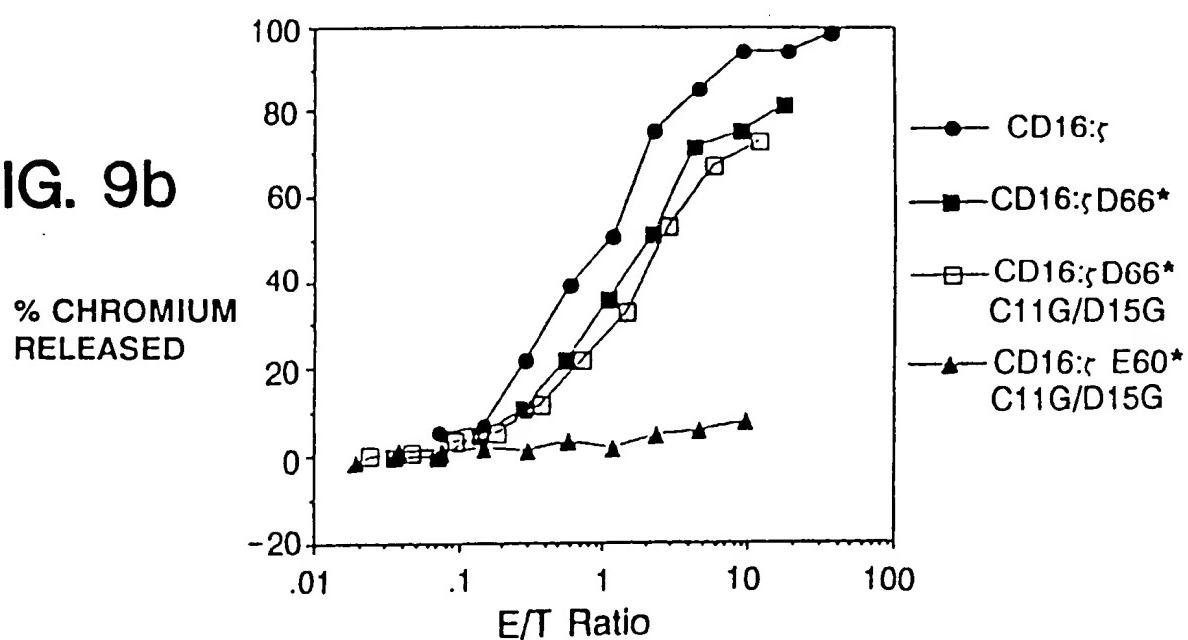
# FIG. 8b



**FIG. 9a**

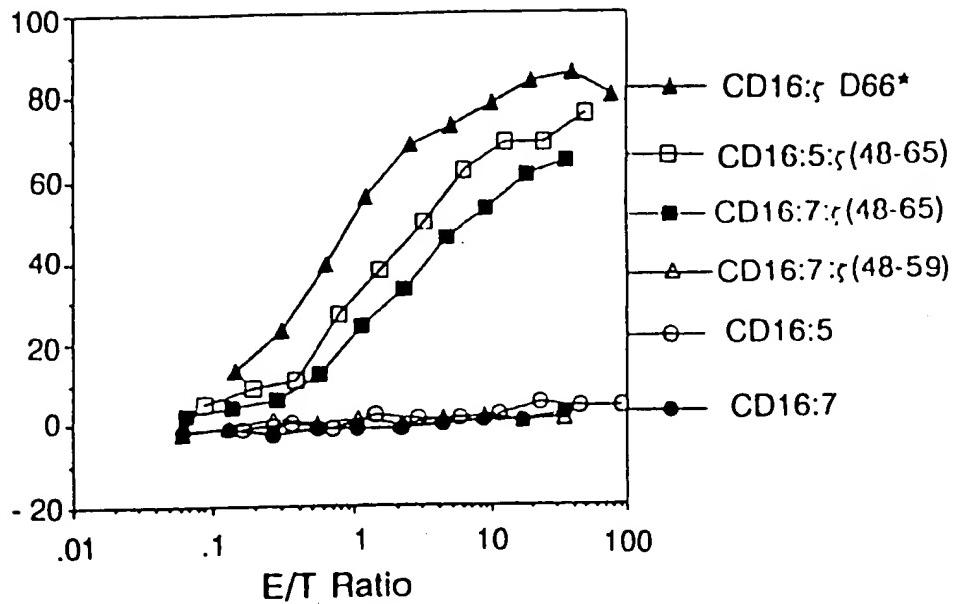


**FIG. 9b**



**FIG. 9c**

100  
80  
60  
40  
20  
0  
-20



**FIG. 9d**

MEAN  
RATIO

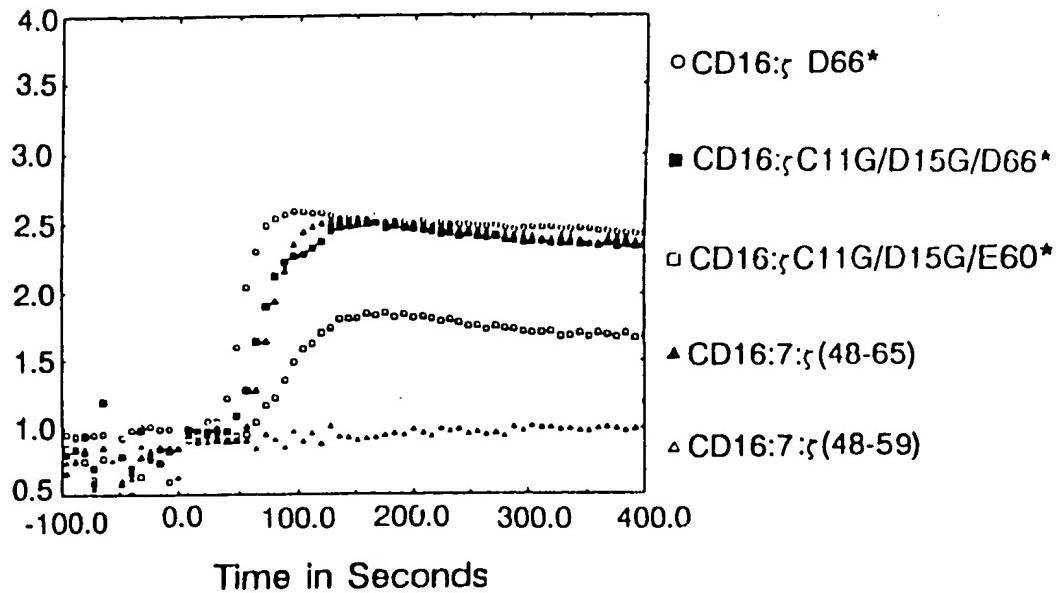


FIG. 10a

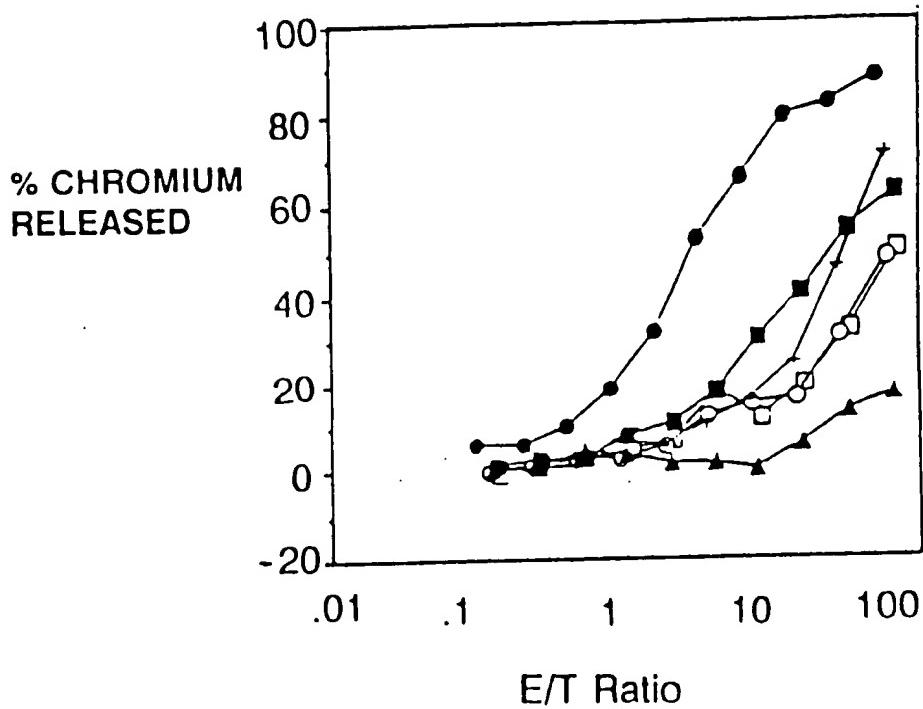
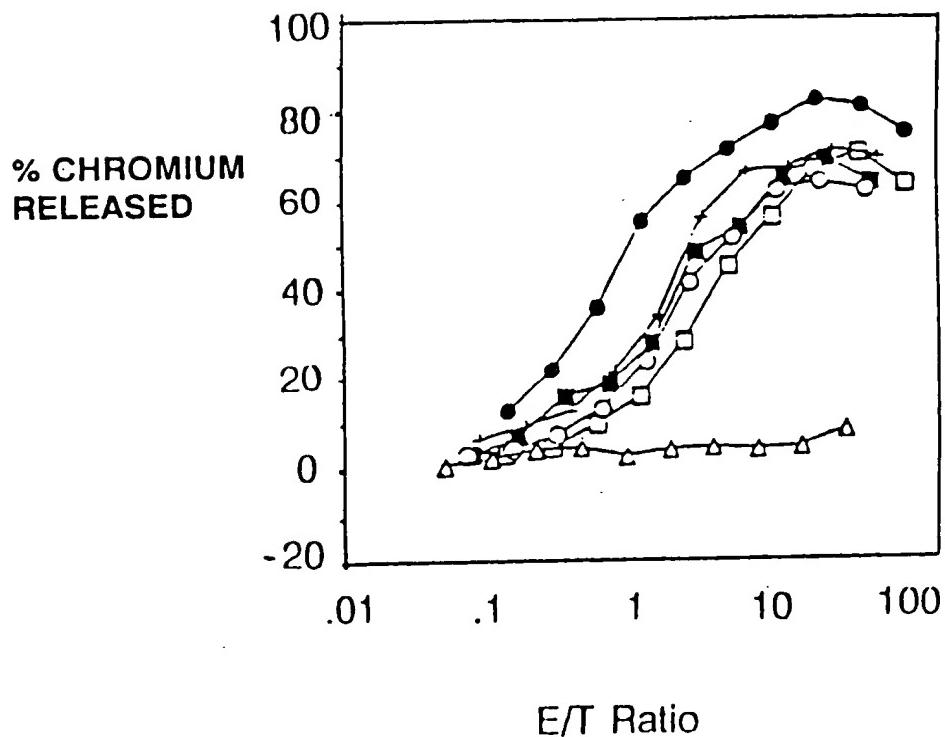
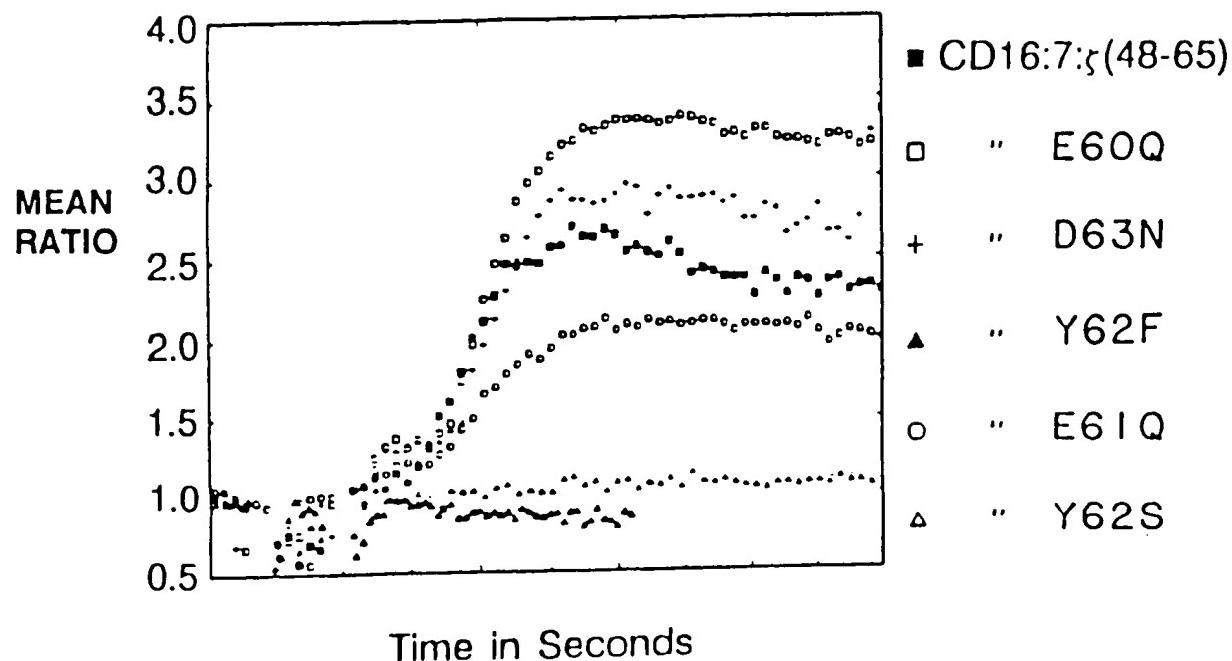


FIG. 10b



DODGE & CO. INC.

FIG. 10c



D63N E60Q E61Q Y62F Y62S CD16:7: $\zeta$ (48-65)

FIG. 10d

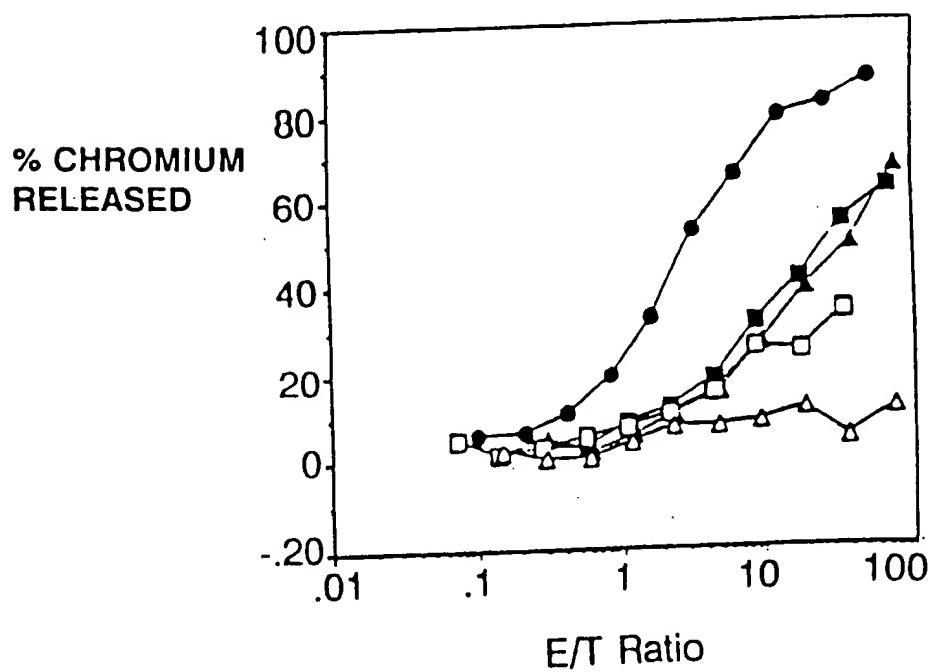


FIG. 10e

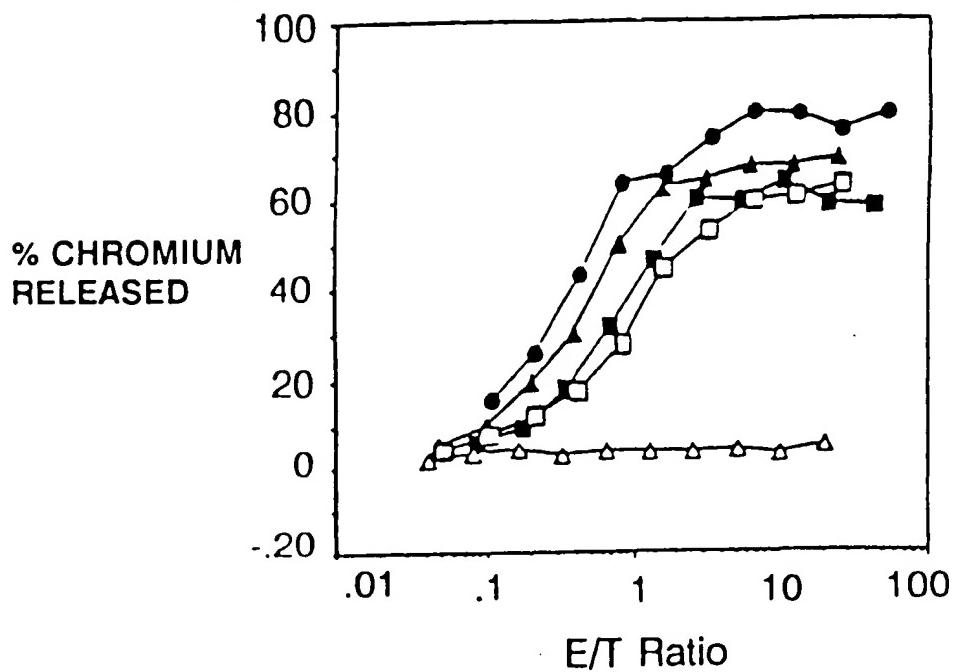
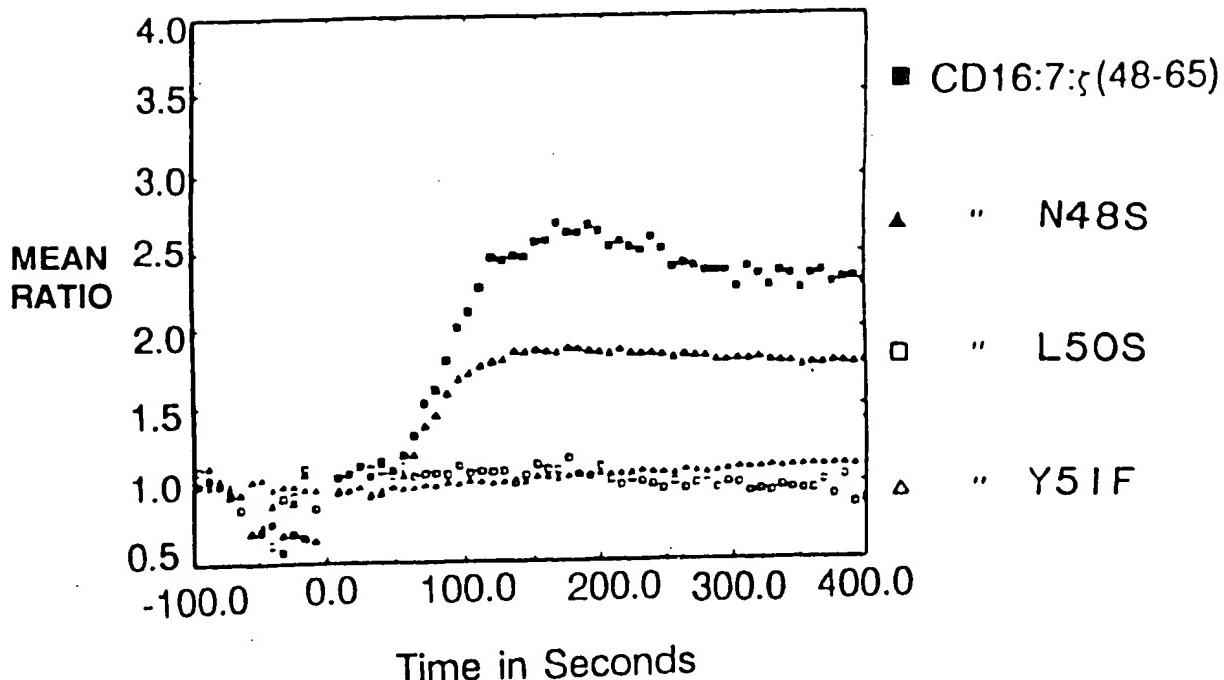
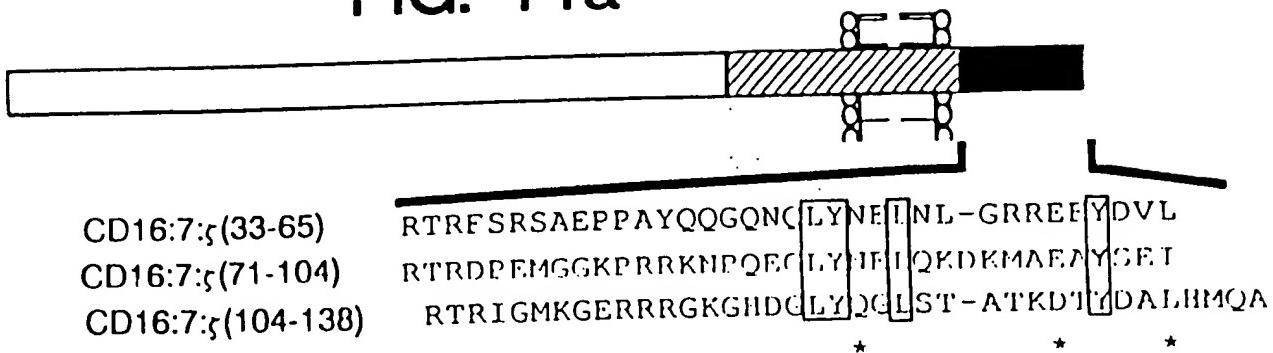


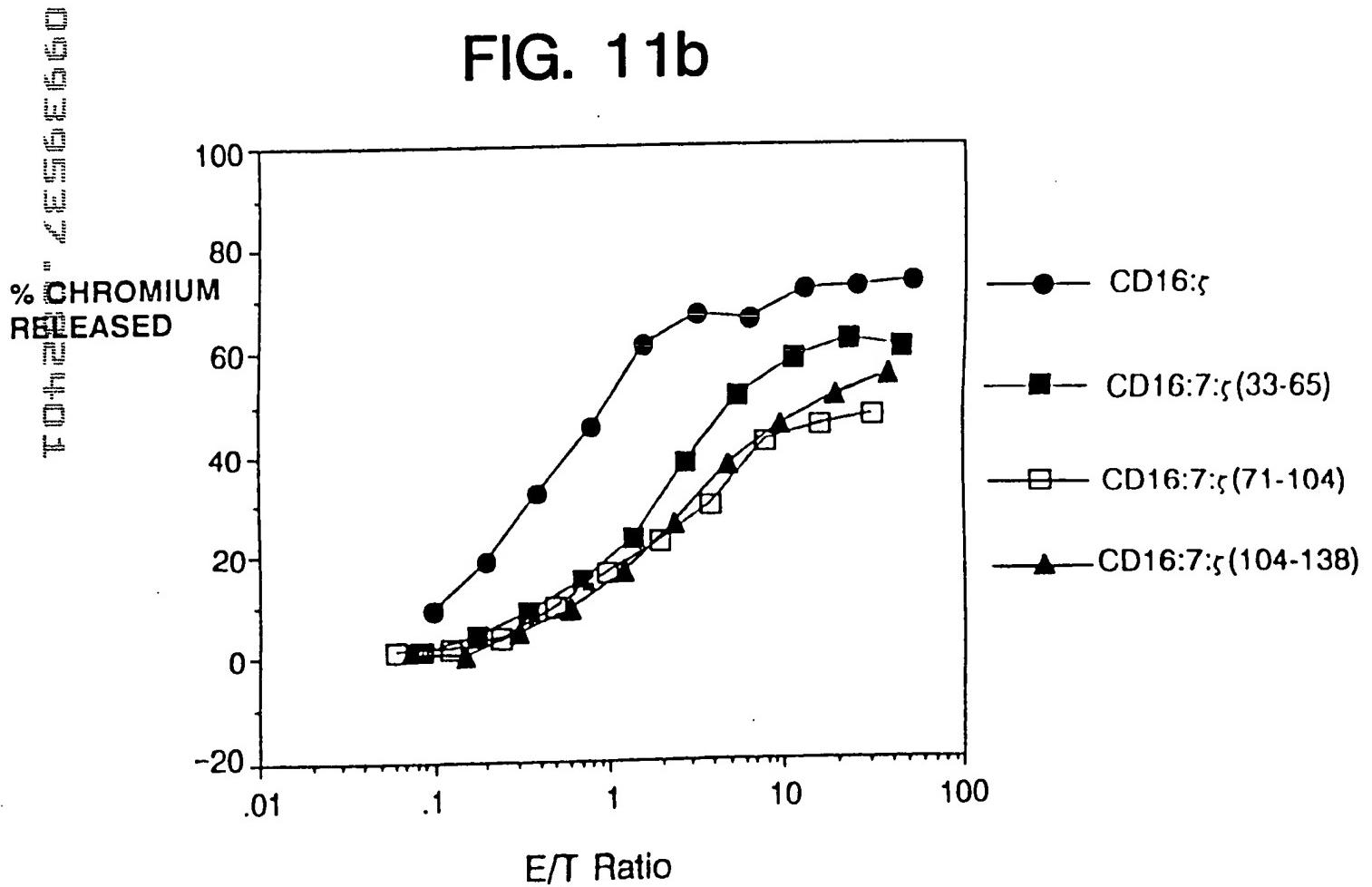
FIG. 10f



**FIG. 11a**



**FIG. 11b**



TOP280-AEAE6E0

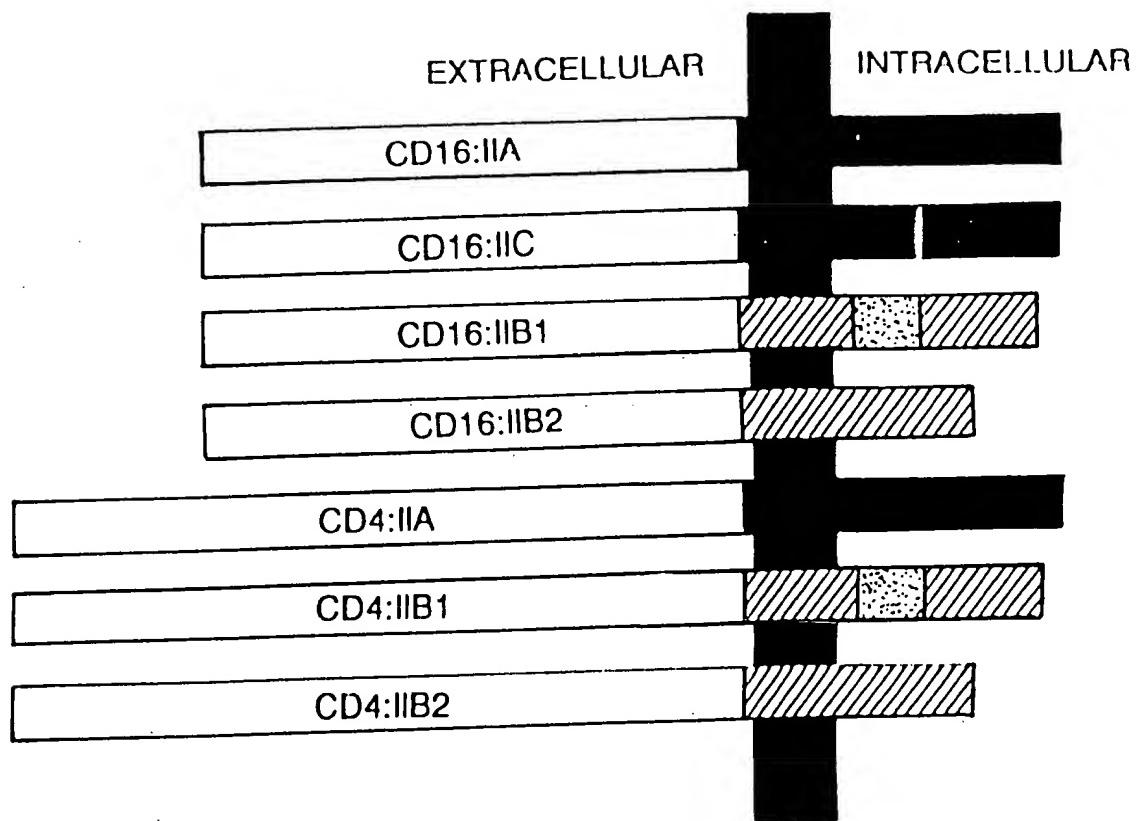
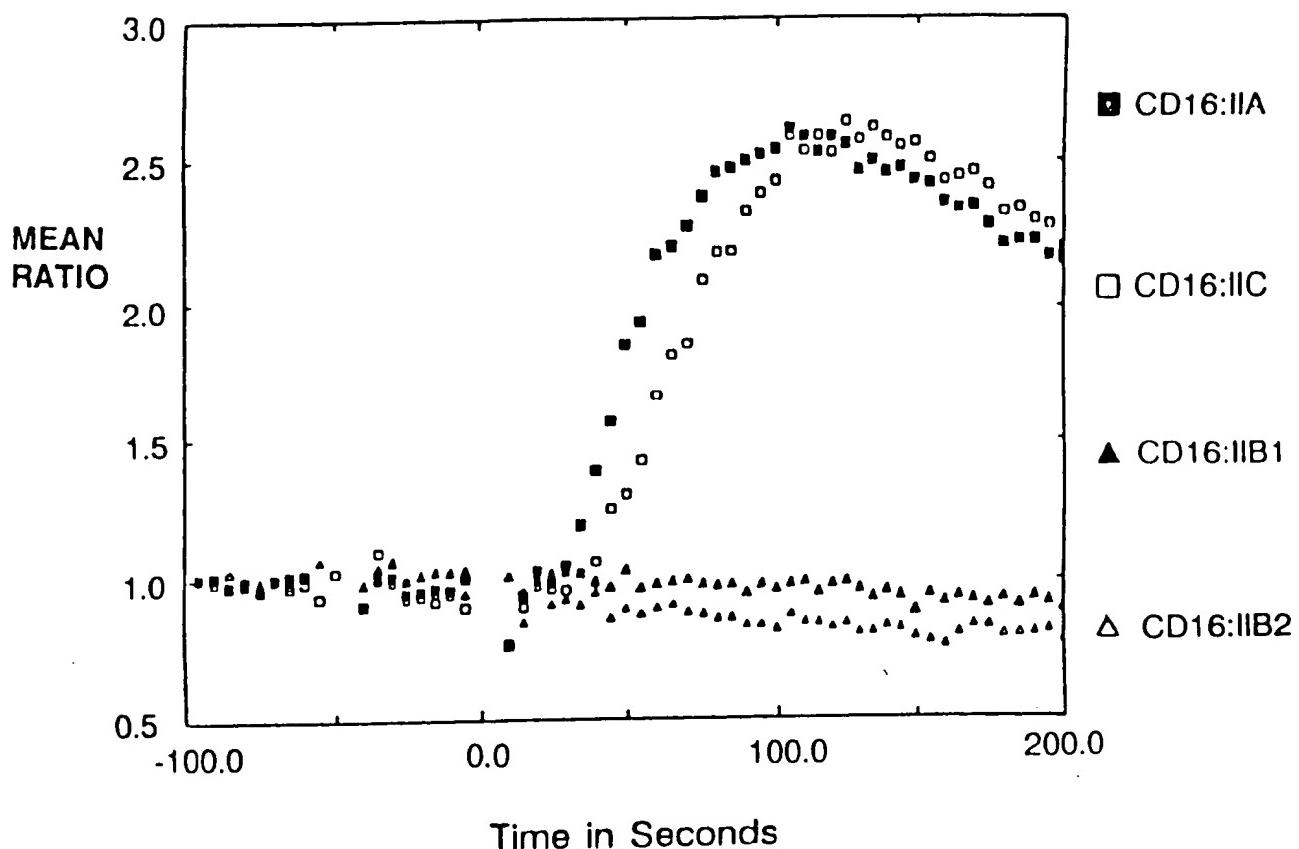


FIG. 12

**FIG. 13a**



**FIG. 13b**

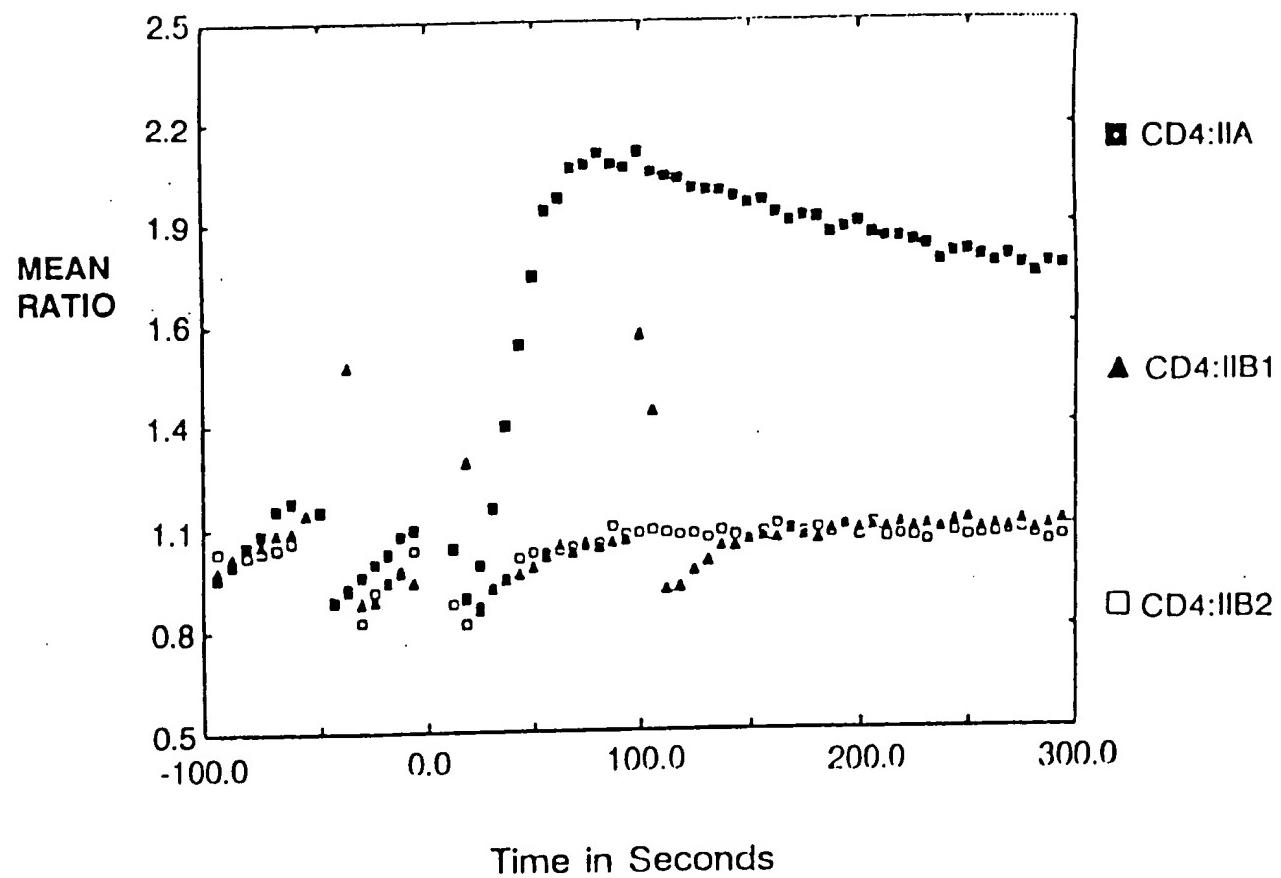


FIG. 14a

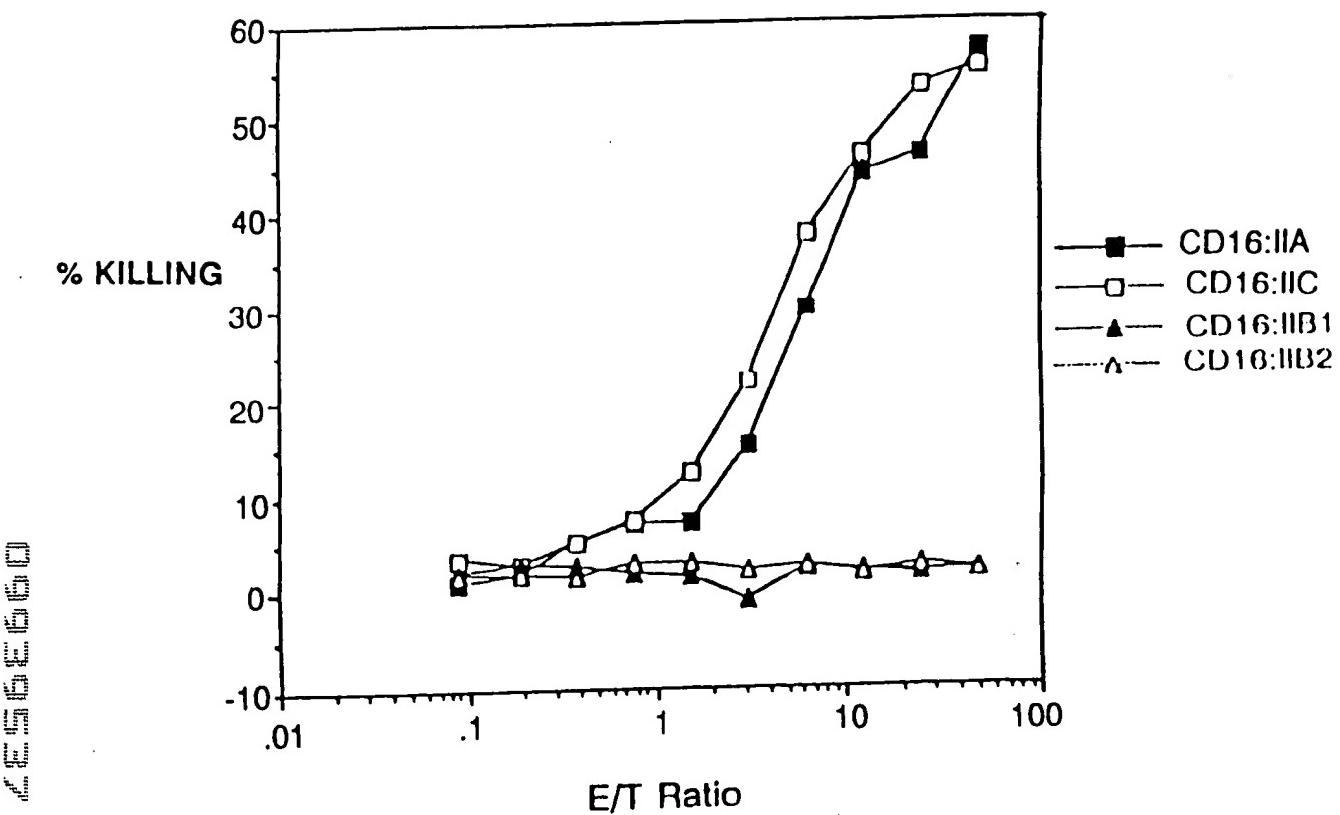
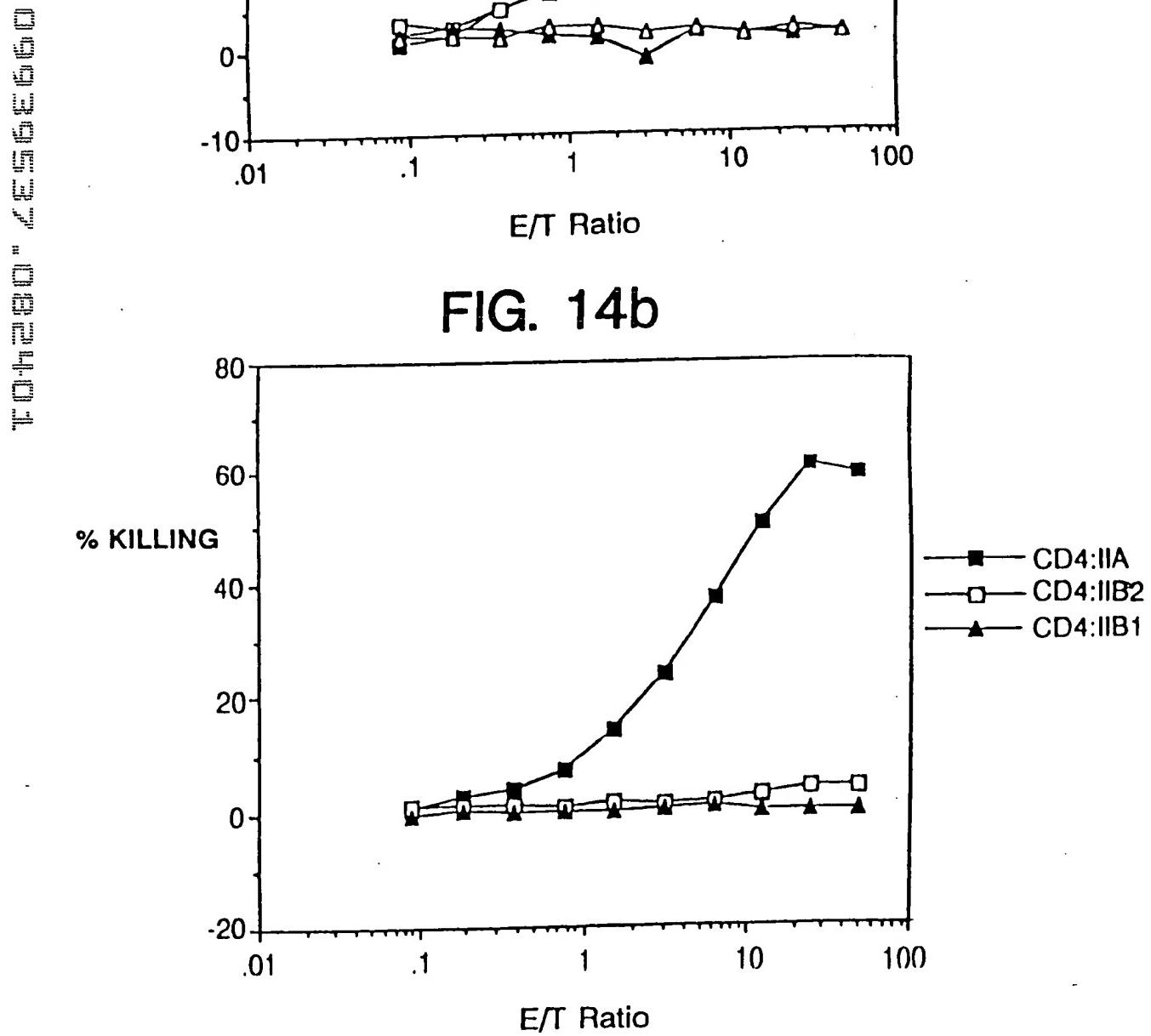
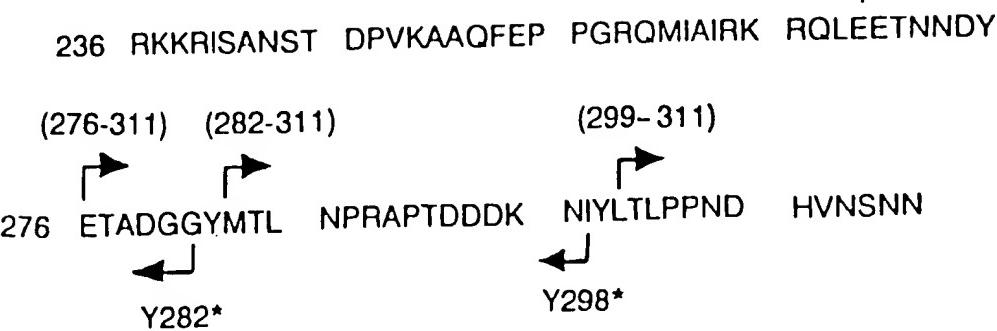


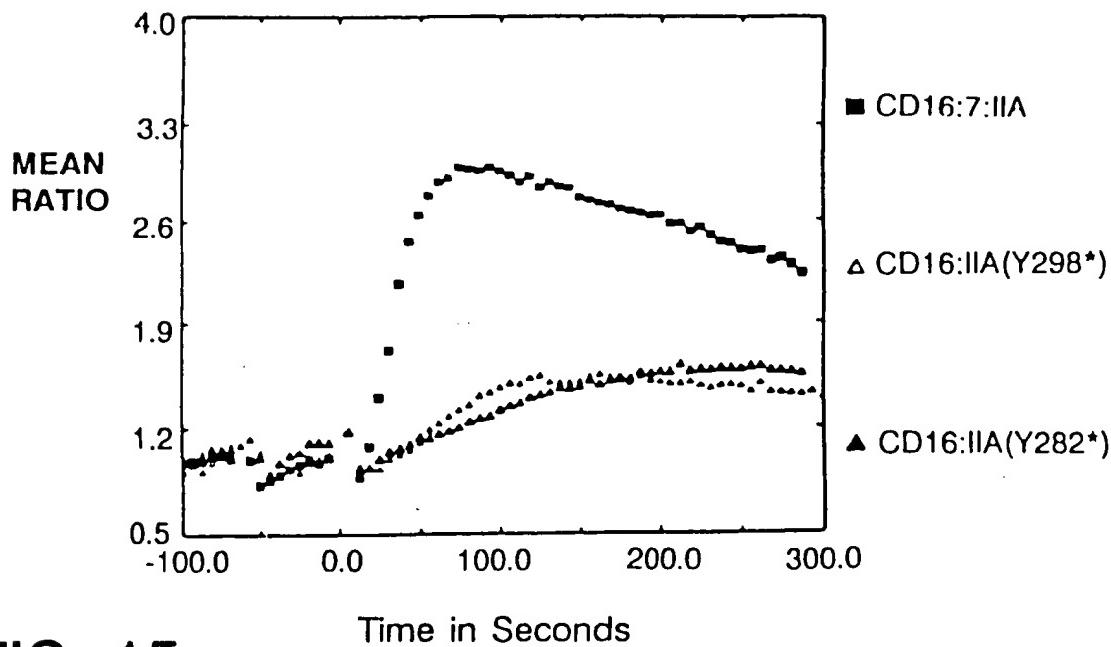
FIG. 14b



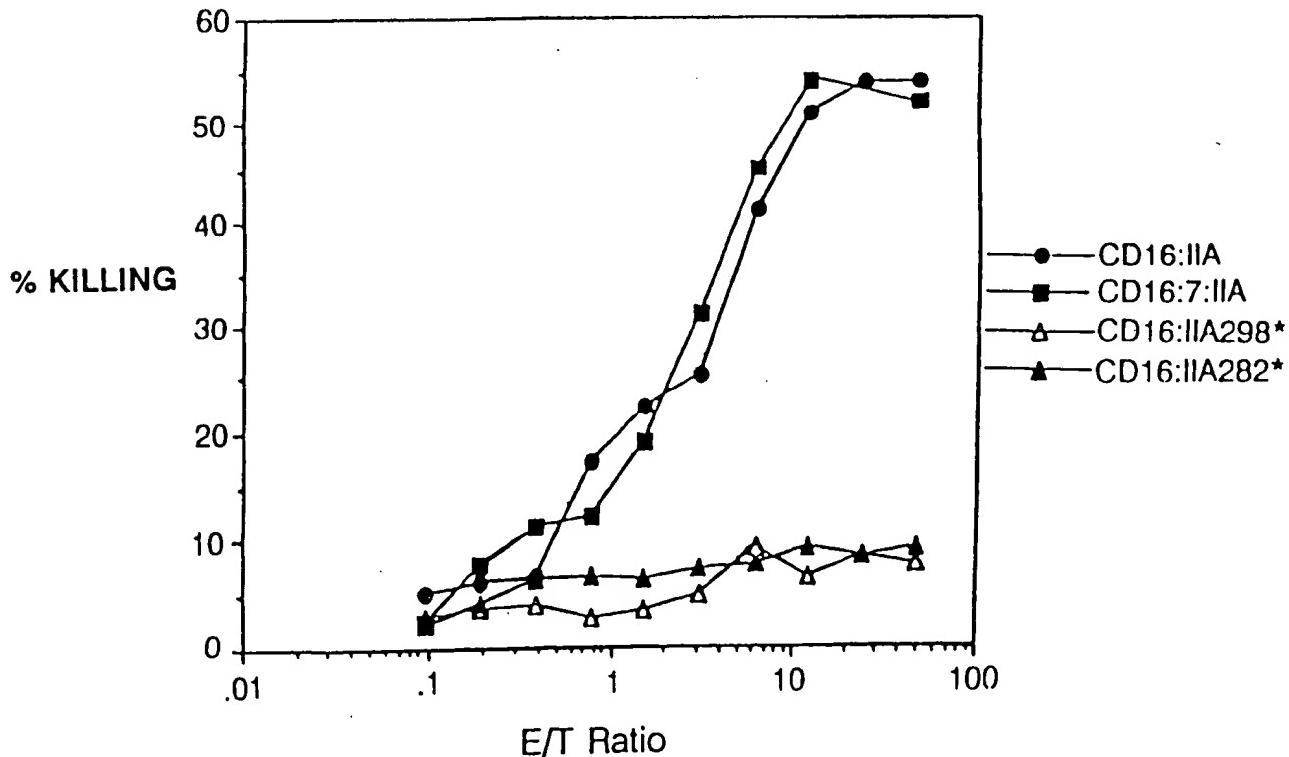
**FIG. 15a**



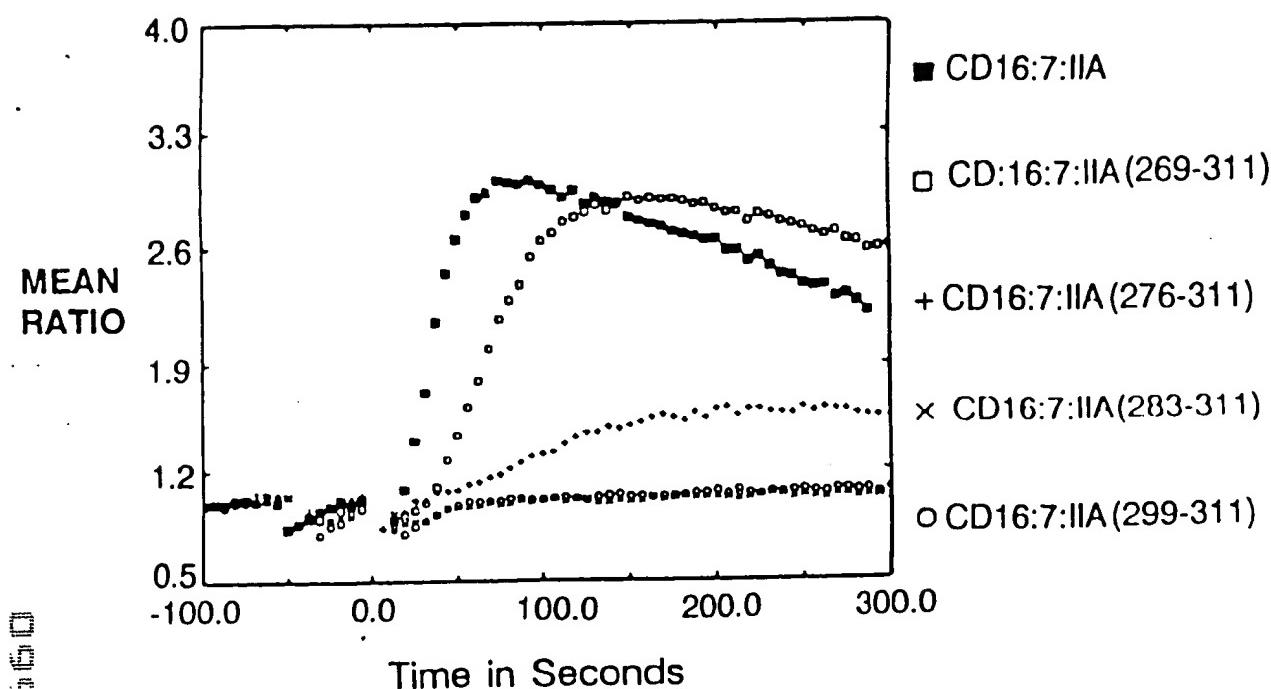
**FIG. 15b**



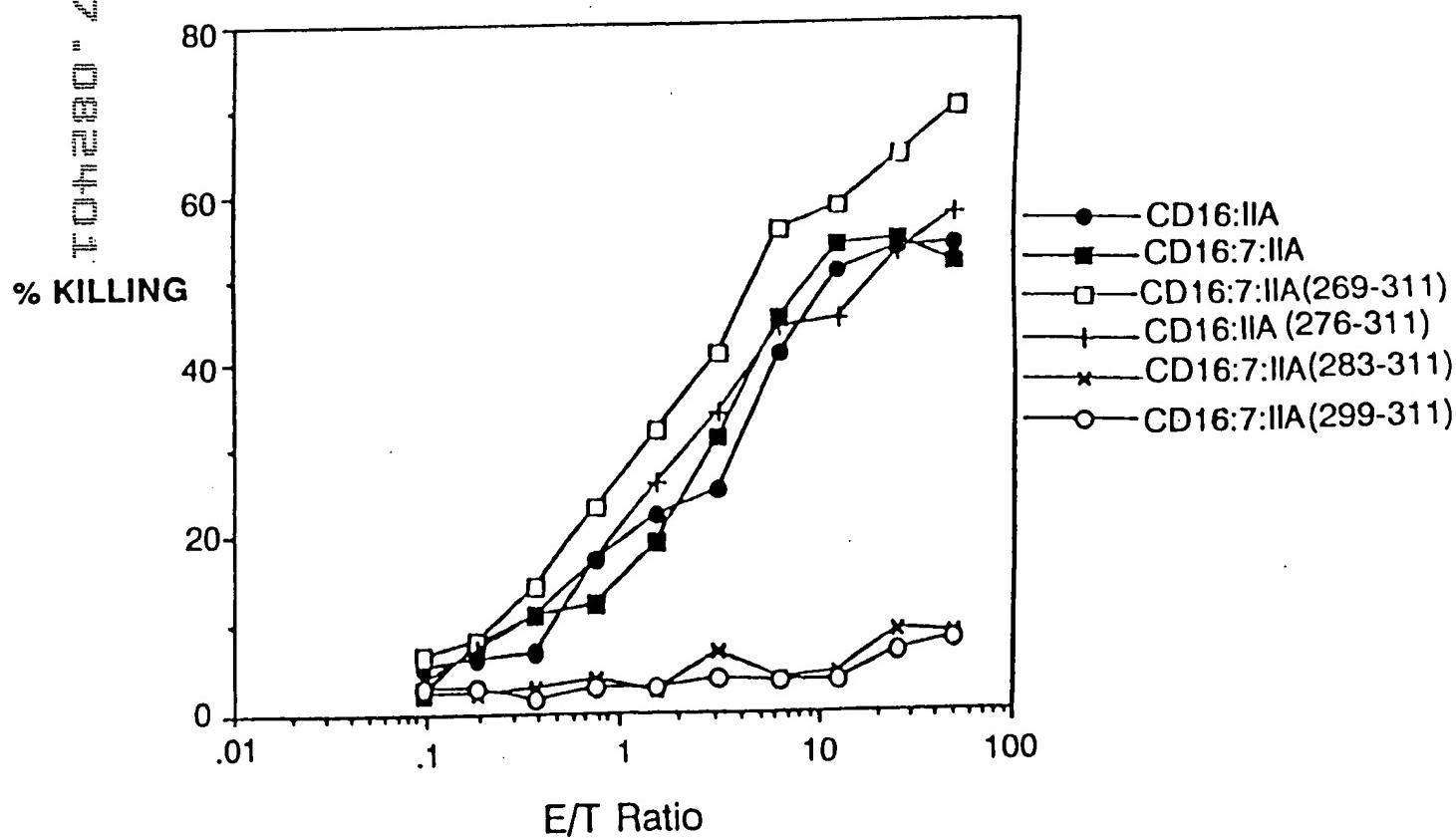
**FIG. 15c**



**FIG. 15d**



**FIG. 15e**



**FIG.16** (Seq. ID No: 24)

1	MEHSTFLSGL	VLATLLSQVS	PKIPIEEL	DRVFVNCNTS	ITWVEGTVG
51	LLSDITRLDL	GKRILDPRGI	YRCNGTDIYK	DKESTVQVHY	RMCQSCVELD
101	PATVAGIIVT	DVIATLLLAL	GVFCFAGHET	GRLSGAADTQ	ALLRNDQVYQ
151	PLRDRDDAQY	SHLGGNWARN	K*		

**FIG.17** (Seq ID NO: 25)

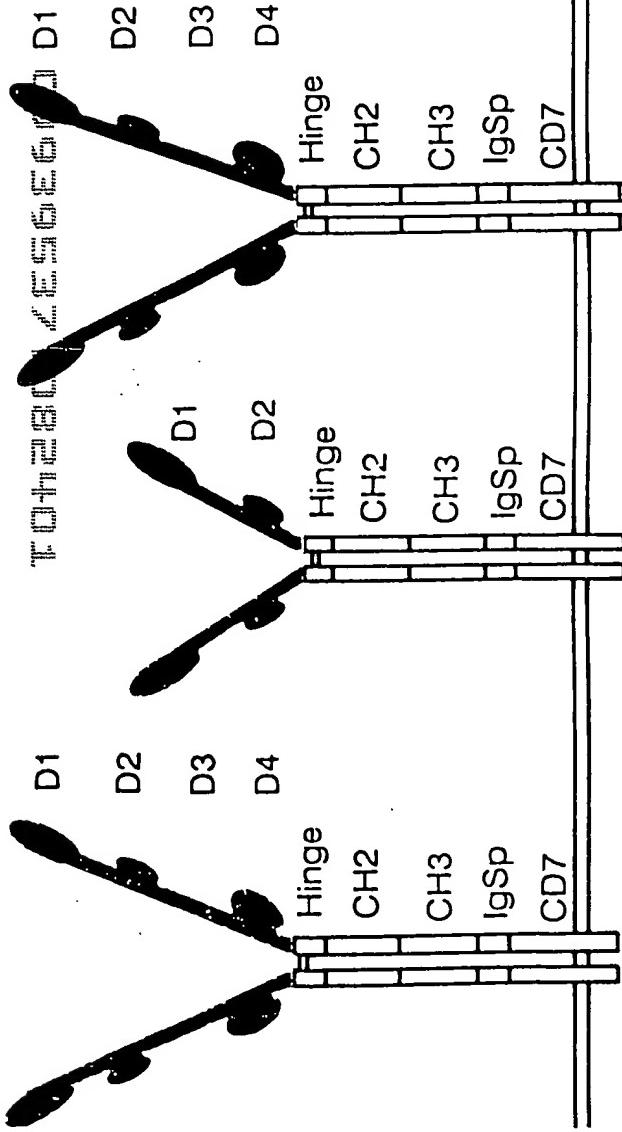
1	MEQGKGLAVL	ILAIIQLQGT	LAQSIKGHNHL	VKVYDYQEDG	SVLLTCDAEA
51	KNITWFKDGK	MIGFLTEDKK	KWNLGSNAKD	PRGMYQCKGS	QNKSKPLQVY
101	YRMCQNCIEL	NAATISGFLF	AEIVSIFVLA	VGVYFIAGQD	GVRQSRASDK
151	QTLLPNDQLY	QPLKDREDDQ	YSHLQGNQLR	RN*	

**FIG.18** (Seq ID No: 26)

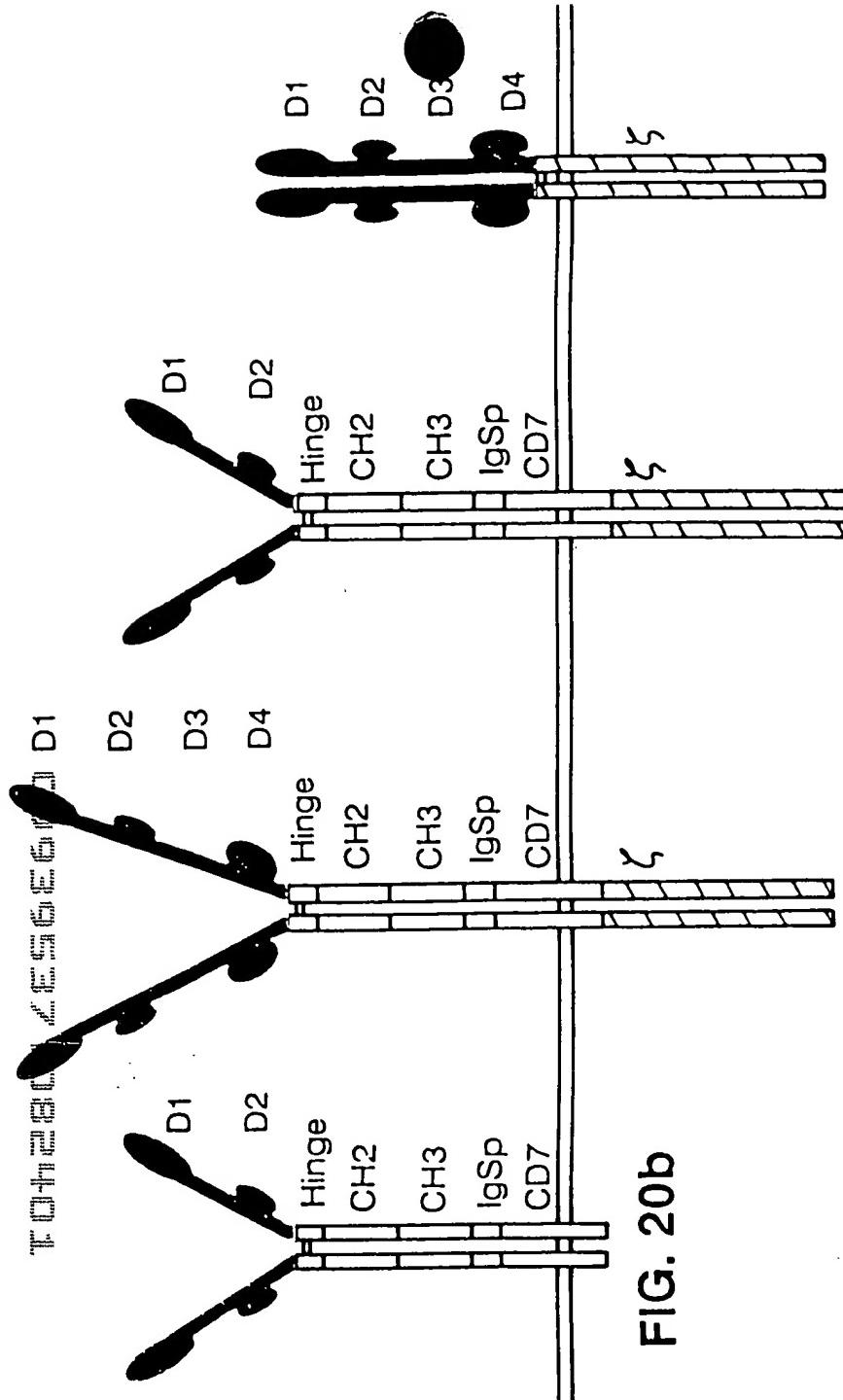
1	MPGGLLEALRA	LPLLLFLSYA	CLGPGCQALR	VEGGPPSLTV	NLGEEARLTC
51	ENNGRNPNT	WWFSLQSNIT	WPPVPLGPGQ	GTTGQLFFPE	VNKNTGACTG
101	CQVIENNILK	RSCGTYLRVR	NPVPRPFLLDM	GEGTKNRIIT	AEGIILLFCA
151	VVPGTLLLFR	KRWQNEKFGV	DMPDDYEDEN	LYEGLNLDDC	SMYEDISRGL
201	QGTYQDVGNL	HIGDAQLEKP	*		

**FIG.19** (Seq ID No: 27)

1	MATLVLSM	CHWLLFL	FSGEPVPAMT	SSDLPLNFQG	SPCSQIWQHP
51	RFAAKKRSSM	VKFHCYT	GALTWFRKRG	SQQPQELVSE	EGRIVQTQNG
101	SVYTLTIQNI	QYEDNGIYFC	KQKCDSANHN	VTDSCGTELL	VLGFSTLDQL
151	KRRNTLKDG	ILIQTLLIIL	FIIVPIFL	DKDDGKAGME	EDHTYEGLNI
201	DQTATYEDIV	TLRTGEVKWS	VGEHPGQE*		



**FIG. 20a**



**FIG. 20b**



**FIG. 20c**



**FIG. 20d**

**FIG. 20e**

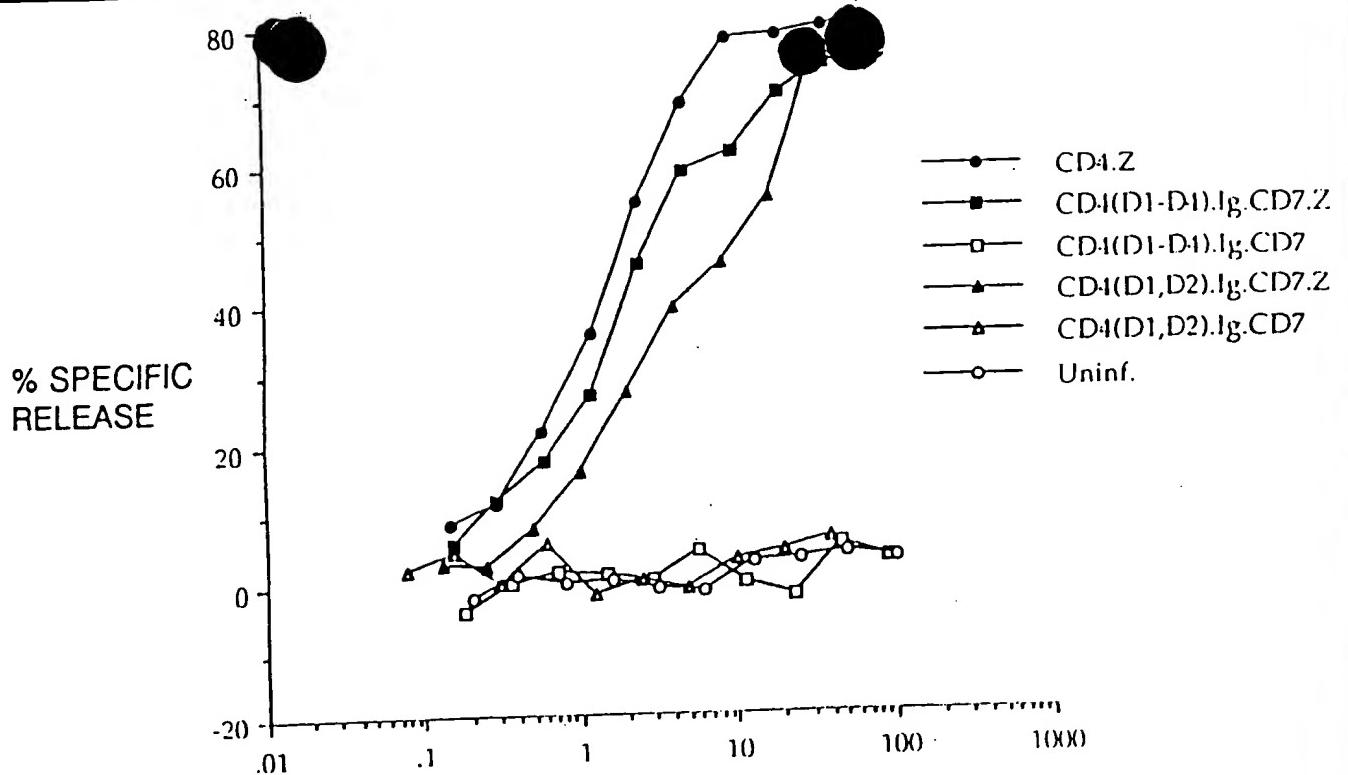
BamHI/BstY1

G GAT CCC AAG GCC AGG CTA AAG CCG AAG CGA AGG CCG AGG CTA AGG CCG AAG CAG ATC TG

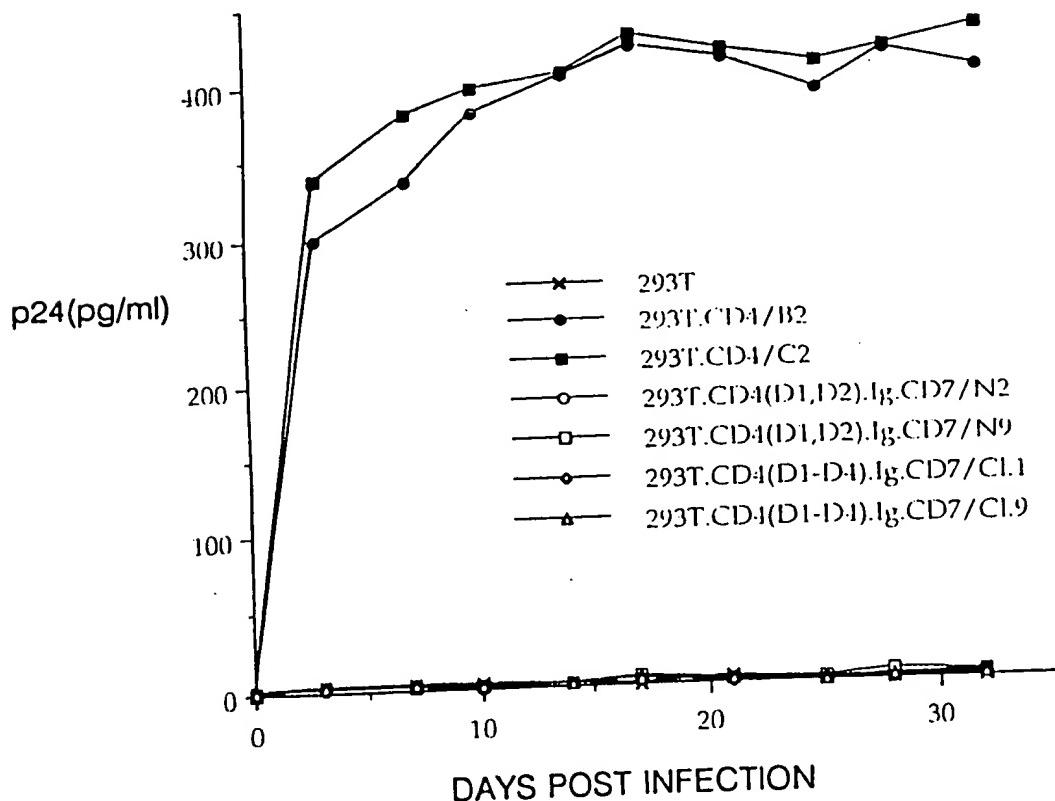
D P K A E A K A E A K A E A D L

**FIG. 28**

BglII/BstY1



EFFECTOR: TARGET  
**FIG. 21**



**FIG. 22**

D1-D4 of CD4

Nucleic Acid Sequence

GCCTGTTGA	GAAGCAGCGG	GCAAGAAAGA	CGCAAGCCCA	GAGGCCCTGC	51
CATTCTGTG	GGCTCAGGTC	CCTACTGGCT	CAGGCCCTG	CCTCCCTCGG	101
CAAGGCCACA	ATGAACCAGGG	GAGTCCCTTT	TAGGCACTTG	CTTCTGGTGC	151
TGCAACTGGC	GCTCCCTCCA	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	201
GGCAAAAAAG	GGGATACAGT	GGAACTGACC	TGTACAGCTT	CCCAGAAGAA	251
GAGCATACAA	TTCCACTGGA	AAAATCCAA	CCAGATAAAAG	ATTCTGGGAA	301
ATCAGGGCTC	CTTCTTAAC	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	351
GAATCAAGAA	GAAGCCTTG	GGACCAAGGA	AACTCCCCC	TGATCATCAA	401
GAATCTTAAG	ATAGAACACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	451
AGAAGGGAGGA	GGTGCAATTG	CTAGTGTTCG	GATTGACTGC	CAACTCTGAC	501
ACCCACCTGC	TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCC	551
TGGTAGTAGC	CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAAACATAC	601
AGGGGGGGAA	GACCCTCTCC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	651
ACCTGGACAT	GCACGTCTT	GCAGAACCAAG	AAGAAGGTGG	AGTTCAAAAT	701
AGACATCGTG	GTGCTAGCTT	TCCAGAAGGC	CTCCAGCATA	GTCTATAAGA	751
AAGAGGGGGGA	ACAGGTGGAG	TTCTCCTTCC	CACTCGCCTT	TACAGTTGAA	801
CAAGCTGACGG	GCAGTGGCGA	GCTGTGGTGG	CAGGCGGAGA	GGGCTTCCTC	851
CTCCAAGTCT	TGGATCACCT	TTGACCTGAA	GAACAAGGAA	GTGTCTGTAA	901
AACGGGTTAC	CCAGGACCCCT	AAGCTCCAGA	TGGGCAAGAA	GCTCCCGCTC	951
CACCTCACCC	TGCCCCAGGC	CTTGCCTCAG	TATGCTGGCT	CTGGAAACCT	1001
CACCCCTGGCC	CTTGAAGCGA	AAACAGGAAA	GTTGCATCAG	GAAGTGAACC	1051
TGGTGGTGAT	GAGAGCCACT	CAGCTCCAGA	AAAATTTGAC	CTGTGAGGTG	1101
TGGGGACCCA	CCTCCCCCTAA	GCTGATGCTG	AGCTTGAAAC	TGGAGAACAA	1151
GGAGGCCAAAG	GTCTCGAAGC	GGGAGAAGCC	GGTGTGGGTG	CTGAACCCCTG	1201
AGGCGGGGGAT	GTGGCAGTGT	CTGCTGAGTG	ACTCGGGACA	GGTCCTGCTG	1251
GAATCCAACA	TCAAGGTTCT	GCCCCACATGG	TCCACCCCGG	TGCACGCGGA	1301

CCCC (SEQ ID NO: 28)

Amino Acid Sequence

MNRGVFRHL	LLVLQLALLP	AATQGNKVVL	GKKGDTVELT	CTASQKKSIQ	51
FHWKNSNQIK	ILGNQGSFLT	KGPSKLNDRA	DSRRSLWDQG	NFPLIIKNLK	101
IEDSDTYICE	VEDQKEEVQL	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	151
PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	TWTCTVLQNQ	KKVEFKIDIV	201
VLAFAQKASSI	VYKKEGEQVE	FSFPLAFTVE	KLTGSGELWW	QAERASSSKS	251
WITFDLKNKE	VSVKRVTQDP	KLQMGKKLPL	HTLPQALPQ	YAGSGNLTLA	301
LEAKTGKLHQ	EVNLVVMRAT	QLQKNLTCEV	WGPTSPKML	SLKLENKEAK	351
VSKREKPVWV	LNPEAGMWQC	LLSDSGQVLL	ESNIKVLPTW	STPVHADP	

(SEQ ID NO: 29)

FIG. 23

## D1-D2 of CD4

## Nucleic Acid Sequence

GCCTGTTGA	GAAGCAGCGG	GCAAGAAAGA	CGCAAGCCCA	GAGGCCCTGC	51
CATTTCTGTG	GGCTCAGGTC	CCTACTGGCT	CAGGCCCTG	CCTCCCTCGG	101
CAAGGCCACA	ATGAACCGGG	GAGTCCCTT	TAGGCACTTG	CTTCTGGTGC	151
TGCAACTGGC	GCTCCTCCC	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	201
GGCAAAAAAG	GGGATAACAGT	GGAACTGACC	TGTACAGCTT	CCCAGAAAGAA	251
GAGCATACAA	TTCCACTGGA	AAAACTCCAA	CCAGATAAAG	ATTCTGGGAA	301
ATCAGGGCTC	CTTCTTAAC	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	351
GAATCAAGAA	GAAGCCTTG	GGACCAAGGA	AACTCCCCC	TGATCATCAA	401
GAATCTTAAG	ATAGAACACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	451
AGAAGGAGGA	GGTGCAATTG	CTAGTGTTCG	GATTGACTGC	CAACTCTGAC	501
ACCCACCTGC	TTCAGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCCC	551
TGGTAGTAGC	CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	601
AGGGGGGAA	GACCCTCTCC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	651
ACCTGGACAT	GCACTGTCTT	GCAGAACCAAG	AAGAAGGTGG	AGTTCAAAAT	701
AGACATCGTG	GTGCTAGCT	(SEQ ID NO: 30)			

Amino Acid Sequence

NRGVFPRHL	LLVLQLALLP	AATQGNKVVL	GKKGDTVELT	CTASQKKSIQ	51
HWKNSNQIK	ILGNQGSFLT	KGPSKLNDRA	DSRRSLWDQG	NFPLIINKNLK	101
EDSDTYICE	VEDQKEEVQL	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	151
PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	TWTCTVLQNQ	KKVEFKIDIV	201
VLA (SEQ ID NO: 31)					

FIG. 24

## Hinge, CH<sub>2</sub>, and CH<sub>3</sub> Domains of Human IgG1

### Nucleic Acid Sequence

GCTAGCAGAG	CCCAAATCTT	GTGACAAAAC	TCACACATGC	CCACCGTGCC	51
CAGCACCTGA	ACTCCTGGGG	GGACCGTCAG	TCTTCCTCTT	CCCCCCAAAA	101
CCCAAGGACA	CCCTCATGAT	CTCCCGGACC	CCTGAGGTCA	CATGCGTGGT	151
GGTGGACGTG	AGCCACGAAG	ACCCCTGAGGT	CAAGTTCAAC	TGGTACGTGG	201
ACGGCGTGGA	GGTGCATAAT	GCCAAGACAA	AGCCCGGGGA	GGAGCAGTAC	251
AACAGCACGT	ACCGGGTGGT	CAGCGTCCTC	ACCGTCCTGC	ACCAGGACTG	301
GCTGAATGGC	AAGGAGTACA	AGTGCAGGT	CTCCAACAAA	GCCCTCCCAG	351
CCCCCATCGA	GAAAACCATC	TCCAAAGCCA	AAGGGCAGCC	CCGAGAACCA	401
CAGGTGTACA	CCCTGCCCCC	ATCCCAGGAT	GAGCTGACCA	AGAACCAAGGT	451
CAGCCTGACC	TGCCTGGTCA	AAGGCTTCTA	TCCCAGCGAC	ATCGCCGTGG	501
AGTGGGAGAG	CAATGGGCAG	CCGGAGAACAA	ACTACAAGAC	CACGCCCTCCC	551
GTGCTGGACT	CCGACGGCTC	CTTCTTCCTC	TACAGCAAGC	TCACCGTGGA	601
CAAGAGCAGG	TGGCAGCAGG	GGAACGTCTT	CTCATGCTCC	GTGATGCATG	651
AGGCTCTGCA	CAACCAACTAC	ACGCAGAAGA	GCCTCTCCCT	GTCTCCGGGG	701
CTGCAACTGG	ACGAGACCTG	TGCTGAGGCC	CAGGACGGGG	AGCTGGACGG	751
GCTCTGGACG	ACGGATCC	(SEQ ID NO: 32)			

### Amino Acid Sequence

D	EPKSCDKTHT	CPPCPAPELL	GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	51
V	VSHEDEPEVKF	NWYVDGVVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	101
E	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPREG	PQVYTLPPSR	DELTKNQVSL	151
T	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVVDKS	201
R	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GLQLDETCAE	AQDGELDGLW	251
	TTDP	(SEQ ID NO: 33)				

**FIG. 25**

## CD7 Transmembrane Domain

## Nucleic Acid Sequence

CCAAGGGCCT CTGCCCTCCC TGCCCCACCG ACAGGGCTCCG CCCTCCCTGA 51  
 CCCGCAGACA GCCTCTGCC C TCCCTGACCC GCCAGCAGCC TCTGCCCTCC 101  
 CTGCGGCCCT GGCGGTGATC TCCTTCCTCC TCGGGCTGGG CCTGGGGGTG 151  
 GCGTGTGTGC TGGCGAGGAC GCGT (SEQ ID NO: 34)

## Amino Acid Sequence

PRASALPAPP TGSALPDPQT ASALPDPPAA SALPAALAVI SFLLGLGLGV  
ACVLARTR (SEQ ID NO: 35) 51

FIG. 26



## Zeta Intracellular Domain

## Nucleic Acid Sequence

ACGCCTTC	GCAGGAGCGC	AGAGCCCCC	GCGTACCAGC	AGGGCCAGAA	51
CCAGCTCTAT	AACGAGCTCA	ATCTAGGACG	AAGAGAGGAG	TACGATGTTT	101
TGGACAAGAG	ACGTGGCCGG	GACCCTGAGA	TGGGGGGAAA	GCCGAGAAAGG	151
AAGAACCCCTC	AGGAAGGCCT	GTACAATGAA	CTGCAGAAAG	ATAAGATGGC	201
GGAGGCCTAC	AGTGAGATTG	GGATGAAAGG	CGAGCGCCGG	AGGGGCAAGG	251
GGCACGGATGG	CCTTTACCAAG	GGTCTCAGTA	CAGCCACCAA	GGACACCTAC	301
GACGCCCTTC	ACATGCAGGC	CCTGGCCCCCT	CGCTAAAGCG	GCCGC	

(SEQ ID NO: 36)

### Amino Acid Sequence

TRFSRSAEPP AYQQGQNQLY NELNLGRREE YDVLDKRRGR DPEMGGKPRR 51  
KNPQEGLYNE LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY 101  
DALHMQALPP R (SEQ ID NO: 37)

**FIG. 27**